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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 18:59:56 ; Search time 560 Seconds
(without alignments)

9284.622 Million cell updates/sec

Title: US-10-763-854-1

Perfect score: 1014

Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccccttga 1014

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1014	100.0	1014	14	US-10-023-775B-1
2	1014	100.0	1014	15	US-10-278-141-10
3	1014	100.0	1014	15	US-10-296-081-10
4	1014	100.0	1014	17	US-10-763-854-1
5	1014	100.0	1560	15	US-10-023-634-5
6	1014	100.0	1851	16	US-10-055-569A-7
7	1012.4	99.8	1014	9	US-09-943-798-3
8	1012.4	99.8	1014	10	US-09-885-453-2
9	1012.4	99.8	1014	14	US-10-270-144-1
10	1012.4	99.8	1014	14	US-10-188-405-7
11	1012.4	99.8	1014	15	US-10-079-384-13
12	1012.4	99.8	1014	15	US-10-225-567A-646

13	1012.4	99.8	1014	15	US-10-321-807-27	Sequence 27, Appl
14	1012.4	99.8	1014	16	US-10-344-728-5	Sequence 5, Appl
15	1012.4	99.8	1014	16	US-10-343-650A-13	Sequence 13, Appl
16	1012.4	99.8	1014	17	US-10-321-807-27	Sequence 27, Appl
17	1012.4	99.8	1014	17	US-10-314-048A-27	Sequence 27, Appl
18	1012.4	99.8	1081	15	US-10-010-568-1	Sequence 1, Appl
19	1012.4	99.8	1081	15	US-10-375-157-1	Sequence 1, Appl
20	1012.4	99.8	1414	15	US-10-017-161-525	Sequence 525, App
21	1012.4	99.8	1414	15	US-10-292-798-463	Sequence 463, App
22	1012.4	99.8	9905	14	US-10-270-144-3	Sequence 3, Appl
23	1010.8	99.7	1729	15	US-10-400-991-17	Sequence 17, Appl
24	976.2	96.3	1020	10	US-09-782-974C-85	Sequence 85, Appl
25	829.4	81.8	831	9	US-09-943-798-1	Sequence 1, Appl
26	728	71.8	1313	9	US-09-728-422-1	Sequence 1, Appl
C 27	537.2	53.0	578	10	US-09-782-974C-59	Sequence 59, Appl
C 28	513.4	50.6	526	9	US-09-812-102-40	Sequence 40, Appl
C 29	481.4	47.5	545	16	US-10-276-774-102	Sequence 102, Appl
C 30	332	32.7	2245	16	US-10-344-728-4	Sequence 4, Appl
C 31	189	18.6	657	11	US-09-801-944B-104	Sequence 104, App
C 32	148.6	14.7	2424	15	US-10-225-567A-218	Sequence 218, Appl
C 33	132.8	13.1	1428	14	US-10-270-587-1	Sequence 1, Appl
C 34	132.6	13.1	3055	16	US-10-305-720-1456	Sequence 1456, Ap
C 35	129.6	12.8	1005	10	US-09-875-076-35	Sequence 35, Appl
C 36	129.6	12.8	1005	10	US-09-876-252-37	Sequence 37, Appl
C 37	129.6	12.8	1005	15	US-10-272-983-35	Sequence 35, Appl
C 38	129.6	12.8	1005	15	US-10-393-807-35	Sequence 35, Appl
C 39	129.6	12.8	1005	15	US-10-417-820A-37	Sequence 37, Appl
C 40	129.6	12.8	1005	17	US-10-723-955-37	Sequence 35, Appl
C 41	129.6	12.8	1005	17	US-10-782-596-35	Sequence 35, Appl
C 42	129.6	12.8	1380	15	US-10-225-567A-566	Sequence 566, App
C 43	129.6	12.8	1436	9	US-09-764-886-36	Sequence 36, Appl
C 44	129.6	12.8	1436	10	US-09-764-886-36	Sequence 36, Appl
C 45	129.6	12.8	1436	16	US-10-264-237-1352	Sequence 1352, Ap

ALIGNMENTS

RESULT 1

US-10-023-775B-1

Sequence 1, Application US/10023775B

Publication No. US2003002282A1

GENERAL INFORMATION:

APPLICANT: Pfizer Inc. (EP/GB only)

APPLICANT: Pfizer Inc. (US, JP, EB except GB)

APPLICANT: Fidcock, Mark David

TITLE OF INVENTION: PC10959AGPR

FILE REFERENCE: PC10959AGPR

CURRENT APPLICATION NUMBER: US/10/023,775B

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: GB 0030854.4

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: US 60/260,590

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: US 60/296,660

PRIOR FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: GB 0111031.1

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1014

TYPE: DNA

ORGANISM: Homo sapiens

US-10-023-775B-1

Query Match 100.0%; Score 1014; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 5.3e-294;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATCAGCTGCT 60
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DB 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATCAGCTGCT 60
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QY 61 TTTGGAATTCAGTGTGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB 61 TTTGGAATTCAGTGTGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
QY 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAAGTAGTATACCTTACATTTTC 180
DB 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAAGTAGTATACCTTACATTTTC 180
QY 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240
DB 181 AAAATGAGACCTTGAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATCTG 240
QY 241 CTGTATCTGACAGCCTCCCTTCCTGATCTACTACTATGCGAGTGGCGAAACCTGGATC 300
DB 241 CTGTATCTGACAGCCTCCCTTCCTGATCTACTACTATGCGAGTGGCGAAACCTGGATC 300
QY 301 TTTGAGATTTCAATGTGAAGTTTATCCGCTTCAGCTTCCTCAATTCACCCCAATGAGC 420
DB 301 TTTGAGATTTCAATGTGAAGTTTATCCGCTTCAGCTTCCTCAATTCACCCCAATGAGC 420
QY 361 ATCCTCTTCCTCAGCTGTTTCCAGCATCTTCGCTACTGTCATCATTCACCCCAATGAGC 480
DB 361 ATCCTCTTCCTCAGCTGTTTCCAGCATCTTCGCTACTGTCATCATTCACCCCAATGAGC 480
QY 421 TGCTTTTCCATTCACAAACTCGATGTGCGAGTTGTAGCTGTGCTGTGCTGTGATCAT 480
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QY 481 TCATGGTAGTGTGATTCGAGACCTTTCTTGTATCAATCAACCAAGCAAGCAAGCA 540
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DB 601 ATTTTCACTGCAACTACTTTTCGCTCCCTTGGTGATAGTGAACCTTTGCTATACGAG 660
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DB 721 AGGCTAAACCATCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 780
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DB 841 CATGAAGCTTACATGCTTCTAGACCATTTAGCTGCTGCAACCTTTGGTAACTGTTA 900
QY 901 CTATATGCTGCTGAGCAGCAACTTTCAAGAGGCTGCTGCTCAACAGTGAATGCAAA 960
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DB 961 GTAAGCGGGAACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 2

US-10-278-141-10
; Sequence 10, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyoung Aina M.

APPLICANT: THORNTON, Michael
APPLICANT: LU, Yan
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: GRAUL, Richard
APPLICANT: KHAN, Farrah A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: WALIA, Narinder K.
APPLICANT: NGUYEN, Damiel B.
APPLICANT: YUE, Henry
APPLICANT: HAFALIA, April
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: LAL, Preeti
APPLICANT: REDDY, Roopa
APPLICANT: KALLICK, Deborah A.
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 USA
CURRENT APPLICATION NUMBER: US/10/278,141
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/208,834
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/207,566
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US01/16285
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/205,628
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/206,222
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030138818A1 6575963CB1
US-10-278-141-10

Query Match 100.0%; Score 1014; DB 15; Length 1014;

Best Local Similarity 100.0%; Pred. No. 5.3e-294;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAATGAGCCACTAGACTATTATGCAATGCTTCTGATTTCCCGATTTATGAGCTGCT 60
QY 61 TTTGGAATTCAGTGTGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB 61 TTTGGAATTCAGTGTGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
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DB 301 TTTGAGATTTCAATGTGAAGTTTATCCGCTTCAGCTTCCTCAATTCACCCCAATGAGC 360
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361	ATCCTCTTCTCACCCTGTTTCAGCAATCTTCCGCTACTGTGTGATCAATTCACCCCAATGAGC	420
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Db		
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Db		

RESULT 3

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US-10-296-081-10
; Sequence 10, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 PCT
; CURRENT APPLICATION NUMBER: US/10/296,081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/208,834; 60/208,861
; PRIOR FILING DATE: 2000-05-22; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02

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Db 901 CTATATGCTGCTGTCAGGCACTTTTACAGAGCTGCTGCTCAACAGTGAATGCAAA 960
Qy 961 GTAAAGCGGGAACCTTTGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
Db 961 GTAAAGCGGGAACCTTTGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 4

US-10-763-854-1
; Sequence 1, Application US/10763854
; Publication No. US20040137574A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10959B
; CURRENT APPLICATION NUMBER: US/10/763,854
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: GB 0030854.4
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 10/023,775
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/296,660
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/260,590
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: GB 0111031.1
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-763-854-1

Query Match 100.0%; Score 1014; DB 17; Length 1014;
Best Local Similarity 100.0%; Pred. No. 5.3e-294;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGCAAGTCTGCT 60
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATTATGCAAGTCTGCT 60
Qy 61 TTTGGAAATTCACGTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
Db 61 TTTGGAAATTCACGTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
Qy 121 GGCATTAATCTCTGCTGGGATTTCCAGGGAATGCAAGTATGATGATATCCACTTACATTTTC 180
Db 121 GGCATTAATCTCTGCTGGGATTTCCAGGGAATGCAAGTATGATGATATCCACTTACATTTTC 180
Qy 181 AAAATGAGACCTTGAAGAGAGACCAACATATTATGCTGAACCTTGGCTGCAACAGATCTG 240
Db 181 AAAATGAGACCTTGAAGAGAGACCAACATATTATGCTGAACCTTGGCTGCAACAGATCTG 240
Qy 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTATGCGAGTGGCGGAAACCTGGATC 300
Db 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTATGCGAGTGGCGGAAACCTGGATC 300
Qy 301 TTTGAGATTTTCATGTGTAAGTTTATCCGTTACGTTCCACTTCCACTTCAACTGTATAGAGC 360
Db 301 TTTGAGATTTTCATGTGTAAGTTTATCCGTTACGTTCCACTTCCACTTCAACTGTATAGAGC 360
Qy 361 ATCTCTTCTCCACTGTTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCAATGAGC 420
Db 361 ATCTCTTCTCCACTGTTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCAATGAGC 420
Qy 421 TGTCTTTCCATTACAAAACTCGATGTGCAAGTTGTAGCCTGTGTGCTGTGGTGGATCAT 480

Db 421 TGTCTTTCCATTACAAAACTCGATGTGCAAGTTGTAGCCTGTGTGGTGGTGAATCAT 480
Qy 481 TCACTGTAGCTGTCTTCCGATGACCTTTCTTGATCAATCAACCAACAGACCAACAGA 540
Db 481 TCACTGTAGCTGTCTTCCGATGACCTTTCTTGATCAATCAACCAACAGACCAACAGA 540
Qy 541 TCAGCCTGTCTCGACCTCACCAAGTTCCGATGAACTCAATACTATTAAAGTGGTACAACTTA 600
Db 541 TCAGCCTGTCTCGACCTCACCAAGTTCCGATGAACTCAATACTATTAAAGTGGTACAACTTA 600
Qy 601 ATTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTAGTACACTTTTGTATACACAG 660
Db 601 ATTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTAGTACACTTTTGTATACACAG 660
Qy 661 ATTATCCACACTCTGACCCATGCAACTGCAAGCTGACAGCTGCTTAAAGCAAAAGCAGA 720
Db 661 ATTATCCACACTCTGACCCATGCAACTGCAAGCTGACAGCTGCTTAAAGCAAAAGCAGA 720
Qy 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATATGTTTTTACCCTTCCATATCTTG 780
Db 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATATGTTTTTACCCTTCCATATCTTG 780
Qy 781 AGGCTCAATTCGATCGAATCTCGCTGCTTCAATCAAGTGTGTTCCATGTAGAAATCAGATC 840
Db 781 AGGCTCAATTCGATCGAATCTCGCTGCTTCAATCAAGTGTGTTCCATGTAGAAATCAGATC 840
Qy 841 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACTGTGA 900
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Db 961 GTAAAGCGGGAACCTTTGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 5

US-10-023-634-5
; Sequence 5, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerkhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025

Query Match	100.0%;	Score 1014;	DB 15;	Length 1560;
Best Local Similarity	100.0%;	Prod. No. 6.8e-294;		
Matches 1014;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTTACAGCTGCT	60	
Db	353	ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTTACAGCTGCT	412	
Qy	61	TTTGGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACCTACCTCCCTGTTATTTAT	120	
Db	413	TTTGGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACCTACCTCCCTGTTATTTAT	472	
Qy	121	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGTCAGTAGTAGATATCCACTTACATTTTC	180	
Db	473	GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGTCAGTAGTAGATATCCACTTACATTTTC	532	
Qy	181	AAATGAGACCTTGGAGAGAGAGACCAATCATTTATGCTGAACTTGGCGCTGCACAGATCTG	240	
Db	533	AAATGAGACCTTGGAGAGAGAGACCAATCATTTATGCTGAACTTGGCGCTGCACAGATCTG	592	
Qy	241	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGTCAGTGCAGGAAACTGATC	300	
Db	593	CTGTATCTGACAGCCTCCCTTCTGATTCACCTACTATGTCAGTGCAGGAAACTGATC	652	
Qy	301	TTTGGAGATTTCAATGTGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360	
Db	653	TTTGGAGATTTCAATGTGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	712	
Qy	361	ATCCTCTTCTCACTGTTTTCAGGACTTCCGCTACTGTGTGATCATTCACCAATGAGC	420	
Db	713	ATCCTCTTCTCACTGTTTTCAGGACTTCCGCTACTGTGTGATCATTCACCAATGAGC	772	
Qy	421	TGCTTTTCCATTACAAAACTCGATGTCAGTTGTAGCCTGTGCTGTGGTGTGGATCAIT	480	
Db	773	TGCTTTTCCATTACAAAACTCGATGTCAGTTGTAGCCTGTGCTGTGGTGTGGATCAIT	832	
Qy	481	TCACTGTGTAGTGTTCATTCGATGACCTTCTTGATATCATCAACCAACGAGCAACAGA	540	
Db	833	TCACTGTGTAGTGTTCATTCGATGACCTTCTTGATATCATCAACCAACGAGCAACAGA	892	
Qy	541	TCGCCCTGTCTCGACCTCACAGTTCCGATGAACCTCAATACTATTAAGTGGTCAACCTA	600	
Db	893	TCGCCCTGTCTCGACCTCACAGTTCCGATGAACCTCAATACTATTAAGTGGTCAACCTA	952	
Qy	601	ATTTTGACTGCACTACTTTTCTGCCCTCCCTTGGTGTAGTGACACTTTTCTATACCACG	660	
Db	953	ATTTTGACTGCACTACTTTTCTGCCCTCCCTTGGTGTAGTGACACTTTTCTATACCACG	1012	

;; PRIOR FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: 60/245,315
;; PRIOR FILING DATE: 2000-11-02
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 137
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 1851
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-055-569A-7

Query Match 100.0%; Score 1014; DB 16; Length 1851;
Best Local Similarity 100.0%; Pred. No. 7.5e-294;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60
Db 347 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 406
Qy 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db 407 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 466
Qy 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
Db 467 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 526
Qy 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
Db 527 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 586
Qy 241 CTGTATCTGACGAGCTCCCTTCTGATTCACATCTATGCACTGAGTGGGAAACTGGATC 300
Db 587 CTGTATCTGACGAGCTCCCTTCTGATTCACATCTATGCACTGAGTGGGAAACTGGATC 646
Qy 301 TTTCGAGATTCATGTGTAAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
Db 647 TTTCGAGATTCATGTGTAAGTTTATCGCTTCCATTTCAACCTGTATAGCAGC 706
Qy 361 ATCTCTTCCTCAGCTTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420
Db 707 ATCTCTTCCTCAGCTTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 766
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTGAGCTGTGCTGTGGTGGATCATTT 480
Db 767 TGCTTTTCCATTCACAAACTCGATGTGCACTGTGAGCTGTGCTGTGGTGGATCATTT 826
Qy 481 TCACTGTGTGCTGCAATTCGGATGACCTTCTTGTATFACATCAACCAAGACCAACAGA 540
Db 827 TCACTGTGTGCTGCAATTCGGATGACCTTCTTGTATFACATCAACCAAGACCAACAGA 886
Qy 541 TCAGCTGTCTCGACCTCAGCTTCGATGCACTCAATATCTTAACTGTGATCAACCTTA 600
Db 887 TCAGCTGTCTCGACCTCAGCTTCGATGCACTCAATATCTTAACTGTGATCAACCTTA 946
Qy 601 ATTTTGTGCTCAACTACTTCTGCTCCCTTGGTGTAGTGAACACTTTGCTATACCAAG 660
Db 947 ATTTTGTGCTCAACTACTTCTGCTCCCTTGGTGTAGTGAACACTTTGCTATACCAAG 1006
Qy 661 ATTTTGTGCTCAACTACTTCTGCTCCCTTGGTGTAGTGAACACTTTGCTATACCAAG 720
Db 1007 ATTTTGTGCTCAACTACTTCTGCTCCCTTGGTGTAGTGAACACTTTGCTATACCAAG 1066
Qy 721 AGGCTAACCTTCTGCTACTCTTGTGATTTTGTAGTGTATTTTACCCTTCCATATCTTG 780
Db 1067 AGGCTAACCTTCTGCTACTCTTGTGATTTTGTAGTGTATTTTACCCTTCCATATCTTG 1126
Qy 781 AGGCTAACCTTGTGATCGAATCTCGCTGCTTTCAATCAGTTGTTCAATGAGAATCAGATC 840
Db 1127 AGGCTAACCTTGTGATCGAATCTCGCTGCTTTCAATCAGTTGTTCAATGAGAATCAGATC 1186
Qy 841 CATGAGCTTACATGCTTTCTAGACCATTAGCTGCTCTGCAACACTTTGTTGTAACCTGTTA 900

Db 1187 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTCTGAACACCTTTGGTAACCTGTTA 1246
Qy 901 CTATATGCTGGTGTGTCAGGCAAACTTTTCAGCAGCTGTCTGCTCAACAGTGCAGATGCAAA 960
Db 1247 CTATATGCTGGTGTGTCAGGCAAACTTTTCAGCAGCTGTCTGCTCAACAGTGCAGATGCAAA 1306
Qy 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
Db 1307 GTAAGCGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1360

RESULT 7
US-09-943-798-3
; Sequence 3, Application US/09943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: QG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-798-3

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATCTCTGATTTCCCGGATATGCACTGCT 60
Qy 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db 61 TTTCGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Qy 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
Db 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
Qy 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
Qy 241 CTGTATCTGACGAGCTCCCTTCTGATTCACATCTATGCTGAGTGGGCAAACTGGATC 300
Db 241 CTGTATCTGACGAGCTCCCTTCTGATTCACATCTATGCTGAGTGGGCAAACTGGATC 300
Qy 301 TTTCGAGATTCATGTGTAAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
Db 301 TTTCGAGATTCATGTGTAAGTTTATCGCTTCCATTTCAACCTGTATAGCAGC 360
Qy 361 ATCTCTTCCTCAGCTTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420
Db 361 ATCTCTTCCTCAGCTTTTCAGATCTTCGCTACTGTGTGATCATTCACCCCAATGAGC 420
Qy 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTGAGCTGTGCTGTGGTGGATCATTT 480
Db 421 TGCTTTTCCATTCACAAACTCGATGTGCACTGTGAGCTGTGCTGTGGTGGATCATTT 480
Qy 481 TCACTGTGTGCTGCAATTCGGATGACCTTCTTGTATFACATCAACCAAGACCAACAGA 540
Db 481 TCACTGTGTGCTGCAATTCGGATGACCTTCTTGTATFACATCAACCAAGACCAACAGA 540
Qy 541 TCAGCTGTCTCGACCTCAGCTTCAGGATGAACTCAATAGTATTTAACTGTGTAACACCTTA 600
Db 541 TCAGCTGTCTCGACCTCAGCTTCAGGATGAACTCAATAGTATTTAACTGTGTAACACCTTA 600

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QY 601 ATTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATGATGACATTTTGTCTATACCAAG 660
Db 601 ATTTGACTGCAACTACTTTTCTGCTCCCTTGGTGATGATGACATTTTGTCTATACCAAG 660
QY 661 ATATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
Db 661 ATATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
QY 721 AGGCTAAACCATCTGCTACTCTCTGATTTTAAAGTATGATTTTAAACCTTCCATATCTTG 780
Db 721 AGGCTAAACCATCTGCTACTCTCTGATTTTAAAGTATGATTTTAAACCTTCCATATCTTG 780
QY 781 AGGCTCAATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGAAATCAGATC 840
Db 781 AGGCTCAATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTCAGAAATCAGATC 840
QY 841 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTCTGAAACACTTTGGTAAACCTGTTA 900
Db 841 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTCTGAAACACTTTGGTAAACCTGTTA 900
QY 901 CTATATGTTGGTGGTTCAGGCAAACTTTTCAAGAGGCTGCTCTCAACAGTGAATGCAAA 960
Db 901 CTATATGTTGGTGGTTCAGGCAAACTTTTCAAGAGGCTGCTCTCAACAGTGAATGCAAA 960
QY 961 GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
Db 961 GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 8
US-09-885-453-2
; Sequence 2, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRxl10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA nucleotide sequence
; LOCATION: (1)..(1014)
; OTHER INFORMATION: GPCRxl10 DNA sequence
US-09-885-453-2

Query Match 99.8%; Score 1012.4; DB 10; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCACTGCT 60
Db 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCTGATTTCCCGATATGCACTGCT 60
QY 61 TTTGGAATTCGACTGTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db 61 TTTGGAATTCGACTGTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
QY 121 GGCATTATCTTCTGCTGGGATTTCCAGGCAATGCAATGATGATATCCACTTACATTTTC 180
Db 121 GGCATTATCTTCTGCTGGGATTTCCAGGCAATGCAATGATGATATCCACTTACATTTTC 180
QY 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
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QY 241 CTGTATCTGACAGCCTCCCTTCCCTGATTTCACTACTATGATGATGATGATGATGATGATC 300
Db 241 CTGTATCTGACAGCCTCCCTTCCCTGATTTCACTACTATGATGATGATGATGATGATGATC 300
QY 301 TTTGGAGATTTTCACTGTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATATACGAC 360
Db 301 TTTGGAGATTTTCACTGTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATATACGAC 360
QY 361 ATCTCTTCTCCTCACTGTTTTCAGCATCTTCCGCTACTGCTGTGATCATTCACCCATGAGC 420
Db 361 ATCTCTTCTCCTCACTGTTTTCAGCATCTTCCGCTACTGCTGTGATCATTCACCCATGAGC 420
QY 421 TCGCTTTTCCATTCACAAACTCGATGTCGAGTTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
Db 421 TCGCTTTTCCATTCACAAACTCGATGTCGAGTTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
QY 481 TCACCTGTAGCTGTCTTCCGATGACCTTCTTGATCAGATCAATCAACCAAGAGCAACACAGA 540
Db 481 TCACCTGTAGCTGTCTTCCGATGACCTTCTTGATCAGATCAATCAACCAAGAGCAACACAGA 540
QY 541 TCAGCTGTCTGAGCTTCACTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 600
Db 541 TCAGCTGTCTGAGCTTCACTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 600
QY 601 ATTTTGAAGCTGCAACTTCTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 660
Db 601 ATTTTGAAGCTGCAACTTCTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 660
QY 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
Db 661 ATTATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
QY 721 AGGCTAACCATCTGCTACTCTCTGCTTTCAGTATGTTTTCACCTTCCATATCTTTG 780
Db 721 AGGCTAACCATCTGCTACTCTCTGCTTTCAGTATGTTTTCACCTTCCATATCTTTG 780
QY 781 AGGCTCAATTCGGATCGAATCTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 840
Db 781 AGGCTCAATTCGGATCGAATCTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 840
QY 841 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTGCTGCAACACTTTGGTAAACCTGTTA 900
Db 841 CATGAAGCTTACATCGTTTCTAGACCAATAGCTGCTGCTGCAACACTTTGGTAAACCTGTTA 900
QY 901 CTATATGTTGGTGGTTCAGGCAAACTTTTTCAGAGGCTGCTCTCAACAGTGAATGCAAA 960
Db 901 CTATATGTTGGTGGTTCAGGCAAACTTTTTCAGAGGCTGCTCTCAACAGTGAATGCAAA 960
QY 961 GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
Db 961 GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 9
US-10-270-144-1
; Sequence 1, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
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; ORGANISM: Human
US-10-270-144-1

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Query Match      99.8%; Score 1012.4; DB 14; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013: Conservative 0; Mismatches 1; Indels 0;
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QY	1	ATGAATGAGCCACTAGACTATTTTAGCAAAATGCTTCTGATTTCCCGGATTATGCAAGTGCCT	60
DB	1	ATGAATGAGCCACTAGACTATTTTAGCAAAATGCTTCTGATTTCCCGGATTATGCAAGTGCCT	60
QY	61	TTTGGAATTTGCACTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT	120
DB	61	TTTGGAATTTGCACTGATGAAAAATCCCACTCAAGATGCACTACCTCCCTGTTATTAT	120
QY	121	GGCAATTATCTTCTCGTGGGATTTTCAGGCAATGCACTAGTAGTATCACTTACATTTTC	180
DB	121	GGCAATTATCTTCTCGTGGGATTTTCAGGCAATGCACTAGTAGTATCACTTACATTTTC	180
QY	181	AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTTGAACCTTGGCTGCACAGATCTG	240
DB	181	AAAATGAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTTGGCTGCACAGATCTG	240
QY	241	CTGTATCTGACCGACTCCCTTCTCGATTCACTACTATGCGAGTGGCGGAAAACTGGATC	300
DB	241	CTGTATCTGACCGACTCCCTTCTCGATTCACTACTATGCGAGTGGCGGAAAACTGGATC	300
QY	301	TTTGGAGATTTCAATGTGTAAAGTTTATCGCTTCAGCTTCCATTTCAACTCTGATAGCAGC	360
DB	301	TTTGGAGATTTCAATGTGTAAAGTTTATCGCTTCAGCTTCCATTTCAACTCTGATAGCAGC	360
QY	361	ATCCTCTTCTCACCTGTTTCAGCACTTTCGGCTACTGTGTGATCAATTCACCAATGAGC	420
DB	361	ATCCTCTTCTCACCTGTTTCAGCACTTTCGGCTACTGTGTGATCAATTCACCAATGAGC	420
QY	421	TGCTTTTCCATTCACAAAATCTCGATGTGGAGTTGTAGCTGTGTGTGGTGTGGATCAAT	480
DB	421	TGCTTTTCCATTCACAAAATCTCGATGTGGAGTTGTAGCTGTGTGTGGTGTGGATCAAT	480
QY	481	TCACCTGGTAGCTGCATTTCCGATGACCTTCTTTGATCACATCAACCAACAGGACCAACAGA	540
DB	481	TCACCTGGTAGCTGCATTTCCGATGACCTTCTTTGATCACATCAACCAACAGGACCAACAGA	540
QY	541	TCAGCTGTCTCGACCTCACCAAGTTTCGGATGAATCAATACATTTAAGTGGTACAACTTA	600
DB	541	TCAGCTGTCTCGACCTCACCAAGTTTCGGATGAATCAATACATTTAAGTGGTACAACTTA	600
QY	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTAGTACACTTTGCTATACCAG	660
DB	601	ATTTTGACTGCAACTACTTTCTGCTCCCTTGGTGTAGTAGTACACTTTGCTATACCAG	660
QY	661	ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCACA	720
DB	661	ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTTAAGCAGAAAGCACA	720
QY	721	AGGCTAAACATTTCTGTACTCTTGCATTTTACGTTATGTTTTTACCTTCCATATCTTG	780
DB	721	AGGCTAAACATTTCTGTACTCTTGCATTTTACGTTATGTTTTTACCTTCCATATCTTG	780
QY	781	AGGGTCATTTCCGATCGAATCTCGCTGCTTTCAATCAGTTGTTTCCATTCAGAAATCAGATC	840
DB	781	AGGGTCATTTCCGATCGAATCTCGCTGCTTTCAATCAGTTGTTTCCATTCAGAAATCAGATC	840
QY	841	CATGAAGCTTACATCGTTTTCTAGACCAATTAGCTGTCTGAAACCTTTTGGTAACTGTTTA	900
DB	841	CATGAAGCTTACATCGTTTTCTAGACCAATTAGCTGTCTGAAACCTTTTGGTAACTGTTTA	900
QY	901	CTATATGTGGTGTGAGCGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTAGATGCAAA	960
DB	901	CTATATGTGGTGTGAGCGACAACTTTTCAGCAGGCTGTCTGCTCAACAGTAGATGCAAA	960
QY	961	GTAAGCGGGAAACCTTTCAGCAAGCAAGAAAAATTTAGTTACTTCAACCAACCTTTGA	1014

D^b 961 GTAAGCGGAACCTTGAGCAAGCAAGAAAATTAGTTACTCAACAACCCCTTGA 1014

RESULT 10

US-10-188-405-7
; Sequence 7, Application US/10188405

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; Publication No. US20030082585A1
;
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1el Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR164
; US-10-188-405-7

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Query Match 99.8%: Score 1012.4: DB 14: Length 1014;

Query Match	99.8%;	Secre.	100.0%;	Borgon	99.7%
Best Local Similarity	99.9%;	Secre.	100.0%;	Borgon	99.7%
Best Local Similarity	99.9%;	Secre.	No. 1.6e-293;		
Matches 1013; Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;				

Qy	1	ATGAATGAGCCCTAGACTATTTHAGAAATGCTTCTGATTTCCCGGATTATGCGACTGCT	60
Db	1	ATGAATGAGCCACTAGACTATTTHAGAAATGCTTCTGATTTCCCGGATTATGCGACTGCT	60
Qy	61	TTTGGAAATTGCACGTGATGAAAAATCCCACTCAAGATGCACCTCCCTGTTATTATTAT	120
Db	61	TTTGGAAATTGCATGATGAAAAATCCCACTCAAGATGCACCTCCCTGTTATTATTAT	120
Qy	121	GGCAATTATCTCTCGTGGGATTTCCAGGCAATGACGTAGTGATATCCACTTTACATTTTC	180
Db	121	GSCATATCTCTCGTGGGATTTCCAGGCAATGACGTAGTGATATCCACTTTACATTTTC	180
Qy	181	AAATAGACCTTGGAGAGCAGACCAATCATTTATGTGTGAACCTGGCTGCACAGATCTG	240
Db	181	AAATAGACCTTGGAGAGCAGACCAATCATTTATGCTGAACCTGGCTGCACAGATCTG	240
Qy	241	CTGTATCTGACACGCTCCCTCTCTGATTCACACTACTATGCAGTGGCGAAACTGGATC	300
Db	241	CTGTATCTGACACGCTCCCTCTCTGATTCACACTACTATGCAGTGGCGAAACTGGATC	300
Qy	301	TTTGGAGATTTCAATGTGTAAAGTTTATTCGGCTTCAGCTTCCATTTCAACTGTATAGCAGC	360
Db	301	TTTGGAGATTTCAATGTGTAAAGTTTATTCGGCTTCAGCTTCCATTTCAACTGTATAGCAGC	360
Qy	361	ATCCTCTTCCTCACTGTTTTCAGACATCTTCGGCTACTGTGTGATCAITTACCCATGAGC	420
Db	361	ATCCTCTTCCTCACCTGTTTCAGACATCTTCGGCTACTGTGTGATCAITTACCCATGAGC	420
Qy	421	TGCTTTTCCATTCACAAACTCGATGTGCAGTGTAGCCTGTGCTGTGGTGTGGATCATTT	480
Db	421	TGCTTTTCCATTCACAAACTCGATGTGCAGTGTAGCCTGTGCTGTGGTGTGGATCATTT	480
Qy	481	TCACCTGTAGCTGTCAITTCGGATGACCTTCTTTGATCACATCAACCAACGAGCCACAGA	540
Db	481	TCACCTGTAGCTGTCAITTCGGATGACCTTCTTTGATCACATCAACCAACGAGCCACAGA	540
Qy	541	TCAGCCTGTCTCGACCTCACAGTTTCGGATGAACTCAATATCTATTAAAGTGTACAACCTTA	600
Db	541	TCAGCCTGTCTCGACCTCACAGTTTCGGATGAACTCAATATCTATTAAAGTGTACAACCTTG	600

QY 601 ATTTGAGTCACTACTTTCTGCTCCCTCCCTGGTGATGACATTTGCTATACACG 660
DB 601 ATTTGAGTCACTACTTTCTGCTCCCTCCCTGGTGATGACATTTGCTATACACG 660
QY 661 ATATCCACACTCTGACCCATGAGTCACTGAACTGACAGTGGCTTAAGCAGAAAGCAG 720
DB 661 ATATCCACACTCTGACCCATGAGTCACTGAACTGACAGTGGCTTAAGCAGAAAGCAG 720
QY 721 AGGCTAACCACTCTGCTACTCTCTGCTCCCTGGTGATGACATTTGCTATACACG 780
DB 721 AGGCTAACCACTCTGCTACTCTCTGCTCCCTGGTGATGACATTTGCTATACACG 780
QY 781 AGGCTAACCACTCTGCTACTCTCTGCTCCCTGGTGATGACATTTGCTATACACG 840
DB 781 AGGCTAACCACTCTGCTACTCTCTGCTCCCTGGTGATGACATTTGCTATACACG 840
QY 841 CATGAAGCTTACATCGTTTCTAGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 CATGAAGCTTACATCGTTTCTAGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014
DB 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014

RESULT 11
US-10-079-384-13
; Sequence 13, Application US/10079384
; Publication No. US2003010896A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
; OTHER INFORMATION:
US-10-079-384-13

Query Match 99.8%; Score 1012.4; DB 15; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTTAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
DB 1 ATGATGAGCCACTAGACTATTTAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
QY 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
DB 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
QY 121 GCAATATCTTCTGCTGGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 180
DB 121 GCAATATCTTCTGCTGGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 180
QY 181 AAAATGACCTTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
DB 181 AAAATGACCTTTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240

QY 241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGATC 300
DB 241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGATC 300
QY 301 TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAG 360
DB 301 TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAG 360
QY 361 ATCCCTTCTCCTCACTGTTTCAGCATTTTCGCTACTGTGTGATCATTTACCCAAATGAGC 420
DB 361 ATCCCTTCTCCTCACTGTTTCAGCATTTTCGCTACTGTGTGATCATTTACCCAAATGAGC 420
QY 421 TCCTTTTCCATTCACAAAACCTCGATGTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
DB 421 TCCTTTTCCATTCACAAAACCTCGATGTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
QY 481 TCACCTGGTAGCTGTCAATCCGATGACCTTCTTGTATCACAATCAACCAAGGACCAACAGA 540
DB 481 TCACCTGGTAGCTGTCAATCCGATGACCTTCTTGTATCACAATCAACCAAGGACCAACAGA 540
QY 541 TCAGCTGTCTCGACCTCAACAGTTTCGGATGAACCTCAATCTATTAAAGTGGTACACCTG 600
DB 541 TCAGCTGTCTCGACCTCAACAGTTTCGGATGAACCTCAATCTATTAAAGTGGTACACCTG 600
QY 601 ATTTTGTGCTGCACTACTTTCTGCTCCCTCCCTTGGTGTATGACACTTTGCTATACACG 660
DB 601 ATTTTGTGCTGCACTACTTTCTGCTCCCTCCCTTGGTGTATGACACTTTGCTATACACG 660
QY 661 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAGAAAGCAGCA 720
DB 661 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAGAAAGCAGCA 720
QY 721 AGGCTAACCACTTCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 780
DB 721 AGGCTAACCACTTCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 780
QY 781 AGGCTAACCACTTCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 840
DB 781 AGGCTAACCACTTCTGCTACTCTCTGATTTTACGATGTTTACCTTCCATATCTTG 840
QY 841 CATGAAGCTTACATCGTTTCTAGACCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 CATGAAGCTTACATCGTTTCTAGACCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014
DB 961 GTAAGCGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACACCTTTGA 1014

RESULT 12
US-10-225-567A-646
; Sequence 646, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 646
; LENGTH: 1014

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-646

Query Match 99.8%; Score 1012.4; DB 15; Length 1014;

Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGAATGAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTAATGACAGTCTGCT 60
DB 1 ATGAATGAGCCTAGACTATTTAGCAAAATCTTCTGATTTCCCGGATTAATGACAGTCTGCT 60
QY 61 TTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB 61 TTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAAGTAGTAGTATCCACTTACATTTTC 180
DB 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAAGTAGTAGTATCCACTTACATTTTC 180
QY 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
DB 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
QY 241 CTGTATCTGACCAAGCCTCCCTTCTGATTCACATCACTATGCACTGGCGAAACCTGGATC 300
DB 241 CTGTATCTGACCAAGCCTCCCTTCTGATTCACATCACTATGCACTGGCGAAACCTGGATC 300
QY 301 TTTGAGATTCATGTTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
DB 301 TTTGAGATTCATGTTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
QY 361 ATCTCTTCTTCCCTCAGCTTTTCCAGATCTTCCGCTTACGCTTCCATTTCAACCTGTATAGCAGC 420
DB 361 ATCTCTTCTTCCCTCAGCTTTTCCAGATCTTCCGCTTACGCTTCCATTTCAACCTGTATAGCAGC 420
QY 421 TGCTTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGGTGTGGATCAT 480
DB 421 TGCTTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGGTGTGGATCAT 480
QY 481 TCACCTGTAGCTGTGTCATTCGATGACCTTCTTGTATCAGATCAATCAACCAAGCAGCAAGA 540
DB 481 TCACCTGTAGCTGTGTCATTCGATGACCTTCTTGTATCAGATCAATCAACCAAGCAGCAAGA 540
QY 541 TCAGCTCTCTCGACCTCACCAGTTCGGATGAACCTCAATATTAATGAGTGAACACCTA 600
DB 541 TCAGCTCTCTCGACCTCACCAGTTCGGATGAACCTCAATATTAATGAGTGAACACCTG 600
QY 601 ATTTTGAAGCAACTACTTTCTGCTCCCTTGGTGTAGTACACTTTTGTCTATACACG 660
DB 601 ATTTTGAAGCAACTACTTTCTGCTCCCTTGGTGTAGTACACTTTTGTCTATACACG 660
QY 661 ATTATCCACACTCTGACCCATGGAATGCAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
DB 661 ATTATCCACACTCTGACCCATGGAATGCAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
QY 721 AGGCTAACATCTGCTACTCTCTGATTTTACGATGATTTTATACCTTCCATATCTTG 780
DB 721 AGGCTAACATCTGCTACTCTCTGATTTTACGATGATTTTATACCTTCCATATCTTG 780
QY 781 AGGGTCATTCGATCGAATCTCGCTTCCATCAATCAATGATTTCCATGAGATCAGATC 840
DB 781 AGGGTCATTCGATCGAATCTCGCTTCCATCAATCAATGATTTCCATGAGATCAGATC 840
QY 841 CATGAGCTTACATCGTTTCTAGACCATTTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
DB 841 CATGAGCTTACATCGTTTCTAGACCATTTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
QY 901 CTATATGTGGTGTGAGCAGCAACTTTTCAGAGGCTGTCTGCTCAACAGTGTAGATGCAA 960
DB 901 CTATATGTGGTGTGAGCAGCAACTTTTCAGAGGCTGTCTGCTCAACAGTGTAGATGCAA 960
QY 961 GTAAGCGGAAACCTTGAGCAAGCAAGAAATTAAGTTACTCTCAACACACCTTTGA 1014
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Db 961 GTAAGCGGAAACCTTGAGCAAGCAAGAAATTAAGTTACTCTCAACACACCTTTGA 1014

RESULT 13

US-10-321-807-27

; Sequence 27, Application US/10321807

; Publication No. US20030166148A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruopeng

; APPLICANT: Dang, Huong T.

; APPLICANT: Lowitz, Kevin P.

; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G

; FILE REFERENCE: AREN0086

; CURRENT APPLICATION NUMBER: US/10/321,807

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US/09/714,008

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1999-11-17

; PRIOR APPLICATION NUMBER: PCT/US99/23938

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/166,088

; PRIOR FILING DATE: 1999-11-17

; PRIOR APPLICATION NUMBER: 60/166,099

; PRIOR FILING DATE: 1999-11-17

; PRIOR APPLICATION NUMBER: 60/166,369

; PRIOR FILING DATE: 1999-11-17

; PRIOR APPLICATION NUMBER: 60/171,902

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/171,901

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/171,900

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/181,749

; PRIOR FILING DATE: 2000-02-11

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 133

; SOFTWARE: Patent In version 3.0

; SEQ ID NO 27

; TYPE: DNA

; LENGTH: 1014

; ORGANISM: Homo sapiens

; US-10-321-807-27

Query Match 99.8%; Score 1012.4; DB 15; Length 1014;

Best Local Similarity 99.9%; Pred. No. 1.6e-293;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGAATGAGCCTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTAATGACAGTCTGCT 60
DB 1 ATGAATGAGCCTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTAATGACAGTCTGCT 60
QY 61 TTTGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB 61 TTTGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAAGTAGTAGTATCCACTTACATTTTC 180
DB 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAAGTAGTAGTATCCACTTACATTTTC 180
QY 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
DB 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
QY 241 CTGTATCTGACCAAGCCTCCCTTCTGATTCACATCACTATGCACTGGCGAAACCTGGATC 300
DB 241 CTGTATCTGACCAAGCCTCCCTTCTGATTCACATCACTATGCACTGGCGAAACCTGGATC 300
QY 301 TTTGAGATTCATGTTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
DB 301 TTTGAGATTCATGTTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
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Qy	361	ATCCTCTTCTCGA	CTGCTTTTCAGCATCTTC	CGCTACTGTGTGATCA	TTCACCCCAATGAGC	420	
Db	361	ATCCTCTTCTTCT	CACCTGTTTCAGCATCTTC	CGCTACTGTGTGATCA	TTCACCCCAATGAGC	420	
Qy	421	TGCTTTTCCATT	CAAAACTCGATGTCGAGTTGT	AGCTGTGCTGTGGTGTGGATCA	TTT	480	
Db	421	TGCTTTTCCATT	CAAAACTCGATGTCGAGTTGT	AGCTGTGCTGTGGTGTGGATCA	TTT	480	
Qy	481	TCACGTGTAGTGT	CAATTC	CGATGACCTTCT	TGTATCACATCA	ACCCAAAGACACCA	540
Db	481	TCACGTGTAGTGT	CAATTC	CGATGACCTTCT	TGTATCACATCA	ACCCAAAGACACCA	540
Qy	541	TCAGCTGTCTCG	ACCTCACCAGTT	CGAGTAACTCA	TATTAAGTGGTACAA	CCCTA	600
Db	541	TCAGCTGTCTCG	ACCTCACCAGTT	CGAGTAACTCA	TATTAAGTGGTACAA	CCCTG	600
Qy	601	ATTTTGACTG	CAACTACTTTTCT	GCCTCCCTTGGT	GATGACACTTTGCT	TATACCA	660
Db	601	ATTTTGACTG	CAACTACTTTTCT	GCCTCCCTTGGT	GATGACACTTTGCT	TATACCA	660
Qy	661	ATTATCCACACT	CTGACCCATGG	AGTGC	AACTGACAGCTGCCTT	TAAGCAGAAACACCA	720
Db	661	ATTATCCACACT	CTGACCCATGG	AGTGC	AACTGACAGCTGCCTT	TAAGCAGAAACACCA	720
Qy	721	AGGCTAAACCA	TTCTGCTACTCCTT	TGCATTTTACGTATG	TTTTTACCCCTCCATATCT	TTG	780
Db	721	AGGCTAAACCA	TTCTGCTACTCCTT	TGCATTTTACGTATG	TTTTTACCCCTCCATATCT	TTG	780
Qy	781	AGGCTAATCG	GAATCTCGCT	CGCTGCTTCAAT	CAATGCTTCCAT	TGAGAATCAGATC	840
Db	781	AGGCTAATCG	GAATCTCGCT	CGCTGCTTCAAT	CAATGCTTCCAT	TGAGAATCAGATC	840
Qy	841	CATGAAGCTT	ACATCGTTCT	TGACCACTAGCT	GCTCTGAAACACCTTTG	GTAACTGTTA	900
Db	841	CATGAAGCTT	ACATCGTTCT	TGACCACTAGCT	GCTCTGAAACACCTTTG	GTAACTGTTA	900
Qy	901	CTATATGTGT	GTGTACGCGACAACTT	TTCAGCAGGCTGT	CTCTCAACAGT	CAGATGCAAA	960
Db	901	CTATATGTGT	GTGTACGCGACAACTT	TTCAGCAGGCTGT	CTCTCAACAGT	CAGATGCAAA	960
Qy	961	GTAAAGCGG	GAACCTTGAG	CAAGCAAA	AAATTAGTTACT	CAAAACACCCCTTGA	1014
Db	961	GTAAAGCGG	GAACCTTGAG	CAAGCAAA	AAATTAGTTACT	CAAAACACCCCTTGA	1014

RESULT 14

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US-10-344-728-5
; Sequence 5, Application US/10344728
; Publication No. US20040038879A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y1-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: LIO131 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/344,728
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/224,989
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-728-5

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QY	61	TTTGGAAATTGCATGTAGTAAAAATCCCATCAAGATGCATCTACTCCCTGTTATTAT	120
Db	61	TTTGGAAATTGCATGTAGTAAAAATCCCATCAAGATGCATCTACTCCCTGTTATTAT	120
QY	121	GGCAATTCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATACACTTACATTTTC	180
Db	121	GGCAATTCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATACACTTACATTTTC	180
QY	181	AAAAATGAGACCTTGGAAAGAGCAGACCAATCATTTATGCTGAACCTGGCTGACACATCTG	240
Db	181	AAAAATGAGACCTTGGAAAGAGCAGACCAATCATTTATGCTGAACCTGGCTGACACATCTG	240
QY	241	CTGTATCTGACAGCCTCCCTTCCTGATTCACACTATGCGAGTGCGGGAACATGGATC	300
Db	241	CTGTATCTGACAGCCTCCCTTCCTGATTCACACTATGCGAGTGCGGGAACATGGATC	300
QY	301	TTTGGAGATTTCAATGTGTAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
Db	301	TTTGGAGATTTCAATGTGTAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
QY	361	ATCCTCTTCCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTCACCCATGAGC	420
Db	361	ATCCTCTTCCTCACCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTCACCCATGAGC	420
QY	421	TGCTTTTCCATTCACAAAATCGAGTGCAGTTGTAGCCTGTGCTGGTGGATCATTT	480
Db	421	TGCTTTTCCATTCACAAAATCGAGTGCAGTTGTAGCCTGTGCTGGTGGATCATTT	480
QY	481	TCACTGTGTAGCTGCATTCGGATGACCTTCGTGATCACATCAACCAACAGGACCAACAGA	540
Db	481	TCACTGTGTAGCTGCATTCGGATGACCTTCGTGATCACATCAACCAACAGGACCAACAGA	540
QY	541	TCAGCCTGTCTCGACCTCACAGTTCCGATGAACCTCAATACTATTAAGTGGTACAACTTA	600
Db	541	TCAGCCTGTCTCGACCTCACAGTTCCGATGAACCTCAATACTATTAAGTGGTACAACTTA	600
QY	601	ATTTTGACTGCACACTATTTTCTGCTCCCTTCGGTGTAGTGACACTTTGCTATACCACG	660
Db	601	ATTTTGACTGCACACTATTTTCTGCTCCCTTCGGTGTAGTGACACTTTGCTATACCACG	660
QY	661	ATTATCCACACTCTGACCCATGACCTGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGGA	720
Db	661	ATTATCCACACTCTGACCCATGACCTGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGGA	720
QY	721	AGGCTAACCAATCTGCTACTCTTCGATTTTACGTAATGTTTTTACCTTCCATATCTTG	780
Db	721	AGGCTAACCAATCTGCTACTCTTCGATTTTACGTAATGTTTTTACCTTCCATATCTTG	780
QY	781	AGGGTCATTCCGGATCGAATCTCGCCTGCTTCCATCAGTTGTTTCCATTTGAGAAATCAGATC	840
Db	781	AGGGTCATTCCGGATCGAATCTCGCCTGCTTCCATCAGTTGTTTCCATTTGAGAAATCAGATC	840
QY	841	CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGACACACCTTTGGTAACCTGTTA	900
Db	841	CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGACACACCTTTGGTAACCTGTTA	900
QY	901	CTATATGTGGTGTAGCGCAACACTTTTCAGCAGGCTGCTGTCTCAACAGTGAAGATGCAAA	960
Db	901	CTATATGTGGTGTAGCGCAACACTTTTCAGCAGGCTGCTGTCTCAACAGTGAAGATGCAAA	960
QY	961	GTAAGCGGAAACCTTGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA	1014
Db	961	GTAAGCGGAAACCTTGAGCAAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA	1014

RESULT 15

RESOLUT 13
US-10-343-650A-13
; Sequence 13, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR

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FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343.650A
PRIOR FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1014)
US-10-343-650A-13

Query Match      99.8%; Score 1012.4; DB 16; Length 1014;
Best Local Similarity 99.9%; Pred. No. 1.6e-293;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTATGCGAGCTGCT 60
DB      1  ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGGATTATGCGAGCTGCT 60

QY      61  TTTGGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120
DB      61  TTTGGAAATTCGACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120

QY      121  GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTGAATCCACTTACATTTTC 180
DB      121  GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTGAATCCACTTACATTTTC 180

QY      181  AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG 240
DB      181  AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCCTGCACAGATCTG 240

QY      241  CTGTATCTGACGAGCTCCCTTCCTGATTTCACTACTATGCGAGTGGCGGAAACCTGGATC 300
DB      241  CTGTATCTGACGAGCTCCCTTCCTGATTTCACTACTATGCGAGTGGCGGAAACCTGGATC 300

QY      301  TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGTATAGCAGC 360
DB      301  TTTGGAGATTTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAAACCTGTATAGCAGC 360

QY      361  ATCCCTCTTCCTCACCTGTTTCAGCATCTTCGCTACTGTGATCATTCACCCCAATGAGC 420
DB      361  ATCCCTCTTCCTCACCTGTTTCAGCATCTTCGCTACTGTGATCATTCACCCCAATGAGC 420

QY      421  TGCTTTTCCATTCAAAAACCTCGATGCGAGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB      421  TGCTTTTCCATTCAAAAACCTCGATGCGAGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY      481  TCACCTGGTAGCTGTCAATTCGGATGACCTTTCGATCAATCAACCAAGAGCCAAACAGA 540
DB      481  TCACCTGGTAGCTGTCAATTCGGATGACCTTTCGATCAATCAACCAAGAGCCAAACAGA 540

QY      541  TCAGCTGTCTCGACCTCACCTACCGATGCGAGTGAACCTCAATCTATTAAAGTGGTACACCTA 600
DB      541  TCAGCTGTCTCGACCTCACCTACCGATGCGAGTGAACCTCAATCTATTAAAGTGGTACACCTG 600

QY      601  ATTTTGGACGCAACTACTTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB      601  ATTTTGGACGCAACTACTTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY      661  ATTATCCACACTCTGACCCCTGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCACGA 720
DB      661  ATTATCCACACTCTGACCCCTGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCACGA 720

QY      721  AGGCTAACCATCTCTGCTACTCTTTCATTTTACGATGTTTTCCTTACCTTCCATATCTTG 780
DB      721  AGGCTAACCATCTCTGCTACTCTTTCATTTTACGATGTTTTCCTTACCTTCCATATCTTG 780
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QY      781  AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTGAGATCAGATC 840
DB      781  AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTGAGATCAGATC 840

QY      841  CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTGGAACACCTTTGGTAACTCTTA 900
DB      841  CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTGGAACACCTTTGGTAACTCTTA 900

QY      901  CTATATGTGTGCTGAGCGACAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACAACCTTTGA 960
DB      901  CTATATGTGTGCTGAGCGACAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACAACCTTTGA 960

QY      961  GTAAGCGGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACAACCTTTGA 1014
DB      961  GTAAGCGGGAACCTTTGAGCAAGCAAGAAATAGTTACTCAAAACAACCTTTGA 1014
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Job time : 567 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 16:31:36 ; Search time 580 Seconds
(without alignments)
9177.436 Million cell updates/sec

Title: US-10-763-854-1
Perfect score: 1014
Sequence: 1 atgaatgagccactagacta.....gttactcaaacacccttga 1014

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_23Sep04.*

1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1014	100.0	1014	6	AAD26370 Human G-p
2	1014	100.0	1014	6	AAD34278 Human AXO
3	1014	100.0	1014	6	ABQ78847 Human G-p
4	1014	100.0	1560	6	ABS51730 Human nov
5	1014	100.0	1851	6	ABS51678 DNA encod
6	1012.4	99.8	1014	5	AAS07948 Human CDN
7	1012.4	99.8	1014	6	ABN85630 Human P2Y
8	1012.4	99.8	1014	6	ABK98323 Human pur
9	1012.4	99.8	1014	6	ABK11381 Human pur
10	1012.4	99.8	1014	6	ABZ42876 Human DNA
11	1012.4	99.8	1014	8	ABZ59170 Human TCR
12	1012.4	99.8	1014	8	ABZ42582 Human G p
13	1012.4	99.8	1014	10	ADC25997 Human pur
14	1012.4	99.8	1014	10	ADC25997 Human pur
15	1012.4	99.8	1014	10	AAD61652 Human GPC
16	1012.4	99.8	1014	11	ADL96473 Human G p
17	1012.4	99.8	1014	12	ADM10573 Human P2Y
18	1012.4	99.8	1014	12	ADO29940 Human GPC
19	1012.4	99.8	1029	8	AAD50885 TARZAN DN
20	1012.4	99.8	1081	6	ABS59232 Human G-p
21	1012.4	99.8	1179	8	AAD50883 Human TAR
22	1012.4	99.8	1288	6	ABL56197 Human P2Y

22	1012.4	99.8	1414	10	ADC86010 Human GPC
23	1012.4	99.8	1797	8	AAD50882 Human TAR
24	1012.4	99.8	5435	6	ABL56198 Human P2Y
25	1012.4	99.8	9905	6	AAK98324 Human pur
26	1010.8	99.7	1729	5	AAS08362 Human CDN
27	1010.8	99.7	1729	5	ABV25767 Human pro
28	1010.8	99.7	1729	5	ABV30024 Human pro
29	1010.8	99.7	1729	5	ABV24026 Human pro
30	1010.8	99.7	1729	5	ABV29909 Human pro
31	1010.8	99.7	1729	12	ADH68218 Human G-p
32	1009.4	99.5	1011	6	AAK43942 Human G p
33	1009.4	99.5	1734	10	ADF70590 Orphan re
34	976.2	96.3	1020	4	AAH51011 Human ngp
35	976.2	96.3	1020	6	ABS70244 DNA encod
36	908.4	89.6	990	10	ADC12673 Human GPC
37	829.4	81.8	831	6	ABN85629 Human P2Y
38	735.6	72.5	1014	8	AAD50884 Mouse TAR
39	735.6	72.5	1014	12	ADM10575 Murine P2
40	735.6	72.5	7399	8	AAD50886 Mouse TAR
41	732.6	72.2	1011	12	ADO30230 Mouse GPC
42	728	71.8	1313	4	AAK52430 Human pol
43	722.8	71.3	1014	12	ADM10577 Rat P2Y25
44	560.8	55.3	740	5	ABV15662 Human pro
45	537.2	53.0	578	4	AAH50998 Human ngp

ALIGNMENTS

RESULT 1

AAD26370

ID AAD26370 standard; cDNA; 1014 BP.

XX AC AAD26370;

XX DT 26-MAR-2002 (first entry)

XX DE Human G-protein coupled receptor 2 (GCRC-2) cDNA.

XX KW Human; G-protein coupled receptor 2; cell proliferative disorder;

XX KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;

XX KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;

XX KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;

XX KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;

XX KW acquired immune deficiency syndrome; inflammatory disorder; infection;

XX KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;

XX KW diabetes; obesity; osteoporosis; gene therapy; GCRC-2; ss.

XX OS Homo sapiens.

XX FH Key

XX FT Location/Qualifiers

XX FT 1..1014

XX FT /*tag= a

XX FT /product= "Human GCRC-2 protein"

XX PN WO200187937-A2.

XX XX

XX PD 22-NOV-2001.

XX XX

XX PF 17-MAY-2001; 2001WO-US016285.

XX XX

XX PR 18-MAY-2000; 2000US-0205628P.

XX PR 22-MAY-2000; 2000US-0206222P.

XX PR 25-MAY-2000; 2000US-0207566P.

XX PR 02-JUN-2000; 2000US-0208834P.

XX PR 02-JUN-2000; 2000US-0208861P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX XX

XX PI Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, Graul R;

XX PI Khan FA, Gandhi AR, Walia NK, Nguyen DB, Yue H, Hafalia A;

XX PI Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;

XX XX

DR WPI: 2002-089844/12.
DR P-PSDB; AAE16171.
XX Novel G-protein coupled receptors and polynucleotides useful for
PT diagnosis, treatment and prevention of disorders of cell proliferation,
PT neurological, cardiovascular, metabolic disorders and viral infections.
XX Claim 5; Page 111-112; 115pp; English.
XX The invention relates to human G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. GPCR polypeptides are useful for
CC screening compounds that modulate their activity. They are useful in the
CC diagnosis, prevention and treatment of disorders which include cell
CC proliferative disorders such as arteriosclerosis, hepatitis,
CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
CC lymphoma; neurological disorders such as epilepsy, ischaemic
CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
CC Parkinson's disease, ataxia, multiple sclerosis, bacterial and viral
CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
CC hypertension, vascular tumours, myocardial infarction, hypertensive heart
CC disease, infective endocarditis, cardiomyopathy, myocarditis;
CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
CC fungal, parasitic, protozoal and helminthic infections and trauma;
CC metabolic disorders such as diabetes, obesity and osteoporosis; and viral
CC infections such as infection caused by viral agent classified as
CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are
CC useful as probes for assessing toxicity of test compounds. They are also
CC used in gene therapy. The present sequence is human G-protein coupled
CC receptor 2 (GPCR-2) cDNA
XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;
Query Match 100.0%; Score 1014; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 1.9e-289;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTCTGATTTCCCGATATGACGTGCT 60
DB 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTCTGATTTCCCGATATGACGTGCT 60
QY 61 TTGGAATGCACTGATGAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTAT 120
DB 61 TTGGAATGCACTGATGAAACATCCCACTCAAGATGACATACCTCCCTGTTATTTAT 120
QY 121 GGCATTATCTCTCGTGGGATTTCCAGGAATGCGAGTAGTGATATCCACTTACATTTTC 180
DB 121 GGCATTATCTCTCGTGGGATTTCCAGGAATGCGAGTAGTGATATCCACTTACATTTTC 180
QY 181 AAAATGAGACTTGGAGAGACAGCACCACATTTATGCTGAACCTGCGCTGCACAGATCTG 240
DB 181 AAAATGAGACTTGGAGAGACAGCACCACATTTATGCTGAACCTGCGCTGCACAGATCTG 240
QY 241 CTGTATCTGACAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGCGAAACTGGATC 300
DB 241 CTGTATCTGACAGCTCCCTCTCTGATTCATCTACTATGCGAGTGGCGAAACTGGATC 300
QY 301 TTGGAATTTATGTTAAGTTTATCCGCTTCAGCTTCCATTTCCACCTGTATAGCAGC 360
DB 301 TTGGAATTTATGTTAAGTTTATCCGCTTCAGCTTCCATTTCCACCTGTATAGCAGC 360
QY 361 ATCCTCTTCTCAGCTGTTTCCAGCATCTTCGGTACTGCTGATTCATCCCAATGAGC 420
DB 361 ATCCTCTTCTCAGCTGTTTCCAGCATCTTCGGTACTGCTGATTCATCCCAATGAGC 420
QY 421 TGCCTTTTCCATTCACAAACTCGATGTCAGTTGTAGCCTGTGCTGTGGATCATTT 480

Db 421 TGCCTTTTCCATTCACAAACTCGATGTCAGTTGTAGCCTGTGCTGTGGATCATTT 480
QY 481 TCACCTGTAGTGTGTCATTTCGGATGACCTTCTTGATCACATCAACCAACAGCAACAGA 540
Db 481 TCACCTGTAGTGTGTCATTTCGGATGACCTTCTTGATCACATCAACCAACAGCAACAGA 540
QY 541 TCAGCCTGTCTCGACCTCACACAGTTCGATGAATCAATATCTATTAAGTGTGTAACCTA 600
Db 541 TCAGCCTGTCTCGACCTCACACAGTTCGATGAATCAATATCTATTAAGTGTGTAACCTA 600
QY 601 ATTTTGTAGTCAACTACTTCTGCTCCCTGCTGATGAGTACACTTTTGTATACCAAG 660
Db 601 ATTTTGTAGTCAACTACTTCTGCTCCCTGCTGATGAGTACACTTTTGTATACCAAG 660
QY 661 ATTTTGTAGTCAACTACTTCTGCTCCCTGCTGATGAGTACACTTTTGTATACCAAG 720
Db 661 ATTTTGTAGTCAACTACTTCTGCTCCCTGCTGATGAGTACACTTTTGTATACCAAG 720
QY 721 AGGCTAACCAATCTGCTACTCTGCTGATTTTACGATGTTTACCTTCCATATCTTG 780
Db 721 AGGCTAACCAATCTGCTACTCTGCTGATTTTACGATGTTTACCTTCCATATCTTG 780
QY 781 AGGCTAACCAATCTGCTACTCTGCTGATTTTACGATGTTTACCTTCCATATCTTG 840
Db 781 AGGCTAACCAATCTGCTACTCTGCTGATTTTACGATGTTTACCTTCCATATCTTG 840
QY 841 CATGAAGCTTATCATCTGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
Db 841 CATGAAGCTTATCATCTGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
QY 901 CTATATGTTGTTGTCAGCAGCAACATTTTTCAGAGGCTGCTGCTCAACAGTGTAGATGCAA 960
Db 901 CTATATGTTGTTGTCAGCAGCAACATTTTTCAGAGGCTGCTGCTCAACAGTGTAGATGCAA 960
QY 961 GTAAGCGGGAACCTTTCAGCAGCAACATTTTTCAGAGGCTGCTGCTCAACAGTGTAGATGCAA 1014
Db 961 GTAAGCGGGAACCTTTCAGCAGCAACATTTTTCAGAGGCTGCTGCTCAACAGTGTAGATGCAA 1014

RESULT 2
AAD34278
ID AAD34278 standard; cDNA; 1014 BP.
XX
AC AAD34278;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human AXOR89 (G-protein coupled receptor) cDNA.
XX
KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
KW infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;
KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
KW myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
KW vomiting; psychotic; neurological disorder; anxiety; manic depression;
KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;
KW dementia; dyskinesia; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1. 1014
FT /*tag= a
FT /product= "Human AXOR89 protein"
XX
PN GB2355012-A.
XX
PD 13-FEB-2002.
XX
PF 10-MAY-2001; 2001GB-00011437.
XX
PR 11-MAY-2000; 2000US-00569137.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Elshourbagy N, Shabon U;
 XX WPI; 2002-332558/37.
 DR P-PSDB; AAE21803.
 XX Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
 PT identifying agonists and antagonists in the treatment of diseases
 PT associated with an AXOR89 imbalance, such as cancers, diabetes or asthma.
 XX Claim 2; Page 30; 37pp; English.
 XX The invention relates to an isolated AXOR89 polypeptide (G-protein
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
 CC and polynucleotide encoding the polypeptide, is useful for identifying
 CC agonists and antagonists (or inhibitors) that are potentially useful in
 CC treating conditions associated with an AXOR89 imbalance, such as
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
 CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
 CC syndrome. The polynucleotide sequence may also be used for chromosome
 CC localisation or tissue expression studies. The AXOR89 is used as a
 CC vaccine or to produce fusion proteins. The present sequence is human
 CC AXOR89 cDNA
 XX
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 1.9e-289;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
 Db 1 ATGAATGAGCCACTAGACTATTTAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
 QY 61 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
 Db 61 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
 QY 121 GCAATATCTCTCTGCGGATTTCCAGCAATGCACTAGTATGATATCCACTTACATTTTC 180
 Db 121 GCAATATCTCTCTGCGGATTTCCAGCAATGCACTAGTATGATATCCACTTACATTTTC 180
 QY 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
 Db 181 AAAATGAGACCTTGGAGAGCAGCACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
 QY 241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTACTGTCAGTGGCGAAACCTGGATC 300
 Db 241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTACTGTCAGTGGCGAAACCTGGATC 300
 QY 301 TTTGGAGATTTCACTGTAAGTTATCCGCTTACCTTCCAGCTTCACTTCACTGTATATGACG 360
 Db 301 TTTGGAGATTTCACTGTAAGTTATCCGCTTACCTTCCAGCTTCACTTCACTGTATATGACG 360
 QY 361 ATCCCTTCTCTACCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTTCACTGTATATGACG 420
 Db 361 ATCCCTTCTCTACCTGTTTTCAGCATCTTCCGCTACTGTGTATCATTTCACTGTATATGACG 420
 QY 421 TGTCTTTTCATTCAAAAACTCGATGTCAGTTGTAGCCTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Db 421 TGTCTTTTCATTCAAAAACTCGATGTCAGTTGTAGCCTGTGTGTGTGTGTGTGTGTGTGTGT 480
 QY 481 TCACGTGTAGTGTCTATCCGATGACCTTCTTGATCACAATCAACCAAGGACCAACAGA 540
 Db 481 TCACGTGTAGTGTCTATCCGATGACCTTCTTGATCACAATCAACCAAGGACCAACAGA 540

QY 541 TCAGCCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATACTATTAACTGTTAGTACCACTA 600
 Db 541 TCAGCCTGTCTCGACCTCACCAGTTCCGATGAACCTCAATACTATTAACTGTTAGTACCACTA 600
 QY 601 ATTTTGACTGCAACTACTTTTCTGCTCCCTCCCTTGGTATAGTACACCTTTTCTATACCAAG 660
 Db 601 ATTTTGACTGCAACTACTTTTCTGCTCCCTCCCTTGGTATAGTACACCTTTTCTATACCAAG 660
 QY 661 ATTATCCACACTCTGACCCATGCAAACTGCAAGCTGCCTTAAAGCAGAAAGCAGCA 720
 Db 661 ATTATCCACACTCTGACCCATGCAAACTGCAAGCTGCCTTAAAGCAGAAAGCAGCA 720
 QY 721 AGGCTAACCATCTGCTACTCTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
 Db 721 AGGCTAACCATCTGCTACTCTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
 QY 781 AGGCTCATTCGGATCGAATCTCCCTCTGCTTCAATCAGTTGTTCCATTGAGAATCAGATC 840
 Db 781 AGGCTCATTCGGATCGAATCTCCCTCTGCTTCAATCAGTTGTTCCATTGAGAATCAGATC 840
 QY 841 CATGAAGCTTACATCGTTTCTAGACCATAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
 Db 841 CATGAAGCTTACATCGTTTCTAGACCATAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
 QY 901 CTATATGTTGTTGTCAGCAGCACTTTCAGCAGGCTGCTCTCAACAGTGAATGCAAA 960
 Db 901 CTATATGTTGTTGTCAGCAGCACTTTCAGCAGGCTGCTCTCAACAGTGAATGCAAA 960
 QY 961 GTAAGCGGGAACCTTGCAGCAAGCAAAAGAAATTAGTTACTCAAAACACCTTGA 1014
 Db 961 GTAAGCGGGAACCTTGCAGCAAGCAAAAGAAATTAGTTACTCAAAACACCTTGA 1014

RESULT 3
 ABQ78847
 ID ABQ78847 standard; cDNA; 1014 BP.
 XX
 AC ABQ78847;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human G-protein coupled receptor PFI-019 cDNA.
 XX
 KW Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
 KW anti-inflammatory; cytosolic; cardiovascular; antiallergic; hypotensive;
 KW antiarteriosclerotic; osteopathic; hypertension; asthma;
 KW artherosclerosis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "PFI-019"
 XX
 PN EP1219638-A2.
 XX
 PD 03-JUL-2002.
 XX
 PF 04-DEC-2001; 2001EP-00310136.
 XX
 PR 18-DEC-2000; 2000GB-00030854.
 PR 04-MAY-2001; 2001GB-00011031.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 PI Fidock MD;
 XX
 DR WPI; 2002-521945/56.
 DR P-PSDB; ABB81902.
 XX

PT New G-protein coupled receptor (GPCR) polypeptide with homology to p2Y
PT purinoreceptor, useful for treating e.g. inflammation or cancers in a
PT patient, or for screening GPCR agonists or antagonists for treating these
PT diseases.

XX Claim 1; Page 12; 19pp; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR), and
CC the polynucleotide encoding it. The protein of the invention has
CC neuroprotective, anti-inflammatory, cytoskeletal, cardiovascular,
CC anti-allergic, hypotensive, anti-arteriosclerotic, and osteoprotective
CC activity. The GPCR polypeptide is useful for manufacturing a medicament
CC for treating a patient who needs to upregulate a receptor. Preferably,
CC therapeutically useful areas are hypertension, asthma, and
CC artherosclerosis. The sequence encodes the G-protein coupled receptor of
CC the invention, PFI-019

XX SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1014;

Best Local Similarity 100.0%; Pred. No. 1.9e-289; Indels 0; Gaps 0;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTATGCGAGTGT	60
DB	1	ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTATGCGAGTGT	60
QY	61	TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTTAT	120
DB	61	TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACTCCCTGTTATTTAT	120
QY	121	GCATTATCTTCTCGTGGATTTCCAGCAATGAGTAGTATGATATCCACTTACATTTTC	180
DB	121	GCATTATCTTCTCGTGGATTTCCAGCAATGAGTAGTATGATATCCACTTACATTTTC	180
QY	181	AAATGAGACCTTGGAGAGCAGCACCATTATGCTGAACTGGCCCTGCACAGATCTG	240
DB	181	AAATGAGACCTTGGAGAGCAGCACCATTATGCTGAACTGGCCCTGCACAGATCTG	240
QY	241	CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGGAAAACCTGGATC	300
DB	241	CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGGAAAACCTGGATC	300
QY	301	TTTGGAGATTTCATGTTAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
DB	301	TTTGGAGATTTCATGTTAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC	360
QY	361	ATCCTCTTCTCCTCAGCTTTTCCGCTACTGTGTATCATTTCAACCAATGAGC	420
DB	361	ATCCTCTTCTCCTCAGCTTTTCCGCTACTGTGTATCATTTCAACCAATGAGC	420
QY	421	TGCTTTTCCATTCACAAAACCTGATGCGATTTGAGCTGCTGCTGTGGTGGATCAT	480
DB	421	TGCTTTTCCATTCACAAAACCTGATGCGATTTGAGCTGCTGCTGTGGTGGATCAT	480
QY	481	TCAGTGTAGCTCTCATTCGGATGACCTTCTGATCACAATCAACAGGACCAACAGA	540
DB	481	TCAGTGTAGCTCTCATTCGGATGACCTTCTGATCACAATCAACAGGACCAACAGA	540
QY	541	TCAGCTGTCTGCACTTCCAGCTTCCGATGAACTCAATCACTATTAGTGGTTCACACCTA	600
DB	541	TCAGCTGTCTGCACTTCCAGCTTCCGATGAACTCAATCACTATTAGTGGTTCACACCTA	600
QY	601	ATTTGACGTGCACTACTTTCTGCTCCCTTGGTGTAGTGTGACCTTTGCTATACACG	660
DB	601	ATTTGACGTGCACTACTTTCTGCTCCCTTGGTGTAGTGTGACCTTTGCTATACACG	660
QY	661	ATTATCCACTCTGACCCCTGAGCTGCAAACTGACAGCTGCTTAAAGCAAGACACGA	720
DB	661	ATTATCCACTCTGACCCCTGAGCTGCAAACTGACAGCTGCTTAAAGCAAGACACGA	720
QY	721	AGGCTAACCAATCTGCTACTCTTCTGCAATTTTACGTATGTTTTTACCTTCCATCTTG	780

DB	721	AGGCTAACCAATCTGCTACTCTTCTGCAATTTTACGTATGTTTTTACCTTCCATCTTG	780
QY	781	AGGCTCAATCGATCGAATCTCGCTGCTTTCAATCAGTGTCTGCTCAATGAGATCAGATC	840
DB	781	AGGCTCAATCGATCGAATCTCGCTGCTTTCAATCAGTGTCTGCTCAATGAGATCAGATC	840
QY	841	CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGAAACACCTTTGGTAACTGTTA	900
DB	841	CATGAAGCTTACATCTGTTTCTAGACCAATAGCTGCTCTGAAACACCTTTGGTAACTGTTA	900
QY	901	CTATATGTTGGTCTGAGGACCAACTTTTCAGCAGGCTGCTGCTCAACAGTGAAGTCAAA	960
DB	901	CTATATGTTGGTCTGAGGACCAACTTTTCAGCAGGCTGCTGCTCAACAGTGAAGTCAAA	960
QY	961	GTAAGCGGAACTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA	1014
DB	961	GTAAGCGGAACTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA	1014

RESULT 4

ABS51730

ID ABS51730 standard; cDNA; 1560 BP.

XX ABS51730;

XX 21-OCT-2002 (first entry)

XX Human novel polynucleotide #3.

Human; gene; ss; trauma; viral infection; parasitic infection; addiction;
bacterial infection; Alzheimer's disease; Huntington's disease; anxiety;
Parkinson's disease; behavioural disorder; pain; hair growth disease;
alopecia; pigmentary disorder; inflammatory disorder; arthritis; AIDS;
inflammatory bowel disease; Crohn's disease; cancer; adenocarcinoma;
acquired immunodeficiency syndrome; colon; asthma; hypertension; obesity;
autoimmune disease; diabetes; graft versus host disease; ulcer; bulimia;
anorexia; dementia; gene therapy.

XX Homo sapiens.

XX WO200257452-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US049122.

XX 15-DEC-2000; 2000US-0256025P.

XX 30-JAN-2001; 2001US-0265163P.

XX 02-MAR-2001; 2001US-0272929P.

XX 09-MAR-2001; 2001US-0274864P.

XX 16-MAR-2001; 2001US-0276688P.

XX 22-MAR-2001; 2001US-0277880P.

XX 25-APR-2001; 2001US-0286409P.

XX 31-JUL-2001; 2001US-0309246P.

XX 29-AUG-2001; 2001US-0315600P.

(CURA-) CURAGEN CORP.

XX Shimketa RA, Colman SD, Spytke KA, Ballinger RA, Guo X;

XX Tchernev VT, Shenoy SG, Li L, Ellerman KE, Zerhusen BD;

XX Patturajan M, Casman SJ, Boldog F, Gusev YV, Burgess CE, Edinger S;

XX Gangolli EA, Malyankar UM, Gunther E, Smithson G, Millet I;

XX Gerlach VL;

XX WPI; 2002-590743/63.

XX P-PSDB; ABG70287.

XX Novel polypeptide, designated NOVX for treating or preventing disorders

or symptoms e.g. trauma, Alzheimer's disease, cancers, acquired

immunodeficiency syndrome, asthma and rheumatoid arthritis.

Claim 9; Page 25; 252pp; English.

CC The invention relates to human novel polynucleotides and polypeptides.
 CC The sequences are useful for the treatment, prevention and diagnosis of
 CC disorders such as trauma, viral/parasitic/bacterial infections,
 CC Alzheimer's disease, Huntington's disease, Parkinson's disease,
 CC behavioural disorders, anxiety, addiction, pain, hair growth diseases,
 CC alopecia, pigmentation disorder, inflammatory disorders such as osteo-
 CC and rheumatoid arthritis, inflammatory bowel disease, Crohn's disease,
 CC acquired immunodeficiency syndrome (AIDS), cancers such as colon cancer
 CC and adenocarcinoma, asthma, hypertension, autoimmune disease, diabetes,
 CC obesity, graft versus host disease, ulcer, bulimia, anorexia and
 CC dementia. Sequences ABS51728-ABS51748 represent human novel
 CC polynucleotides of the invention
 XX
 SQ

Query Match 100.0%; Score 1014; DB 6; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 2.4e-289;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCGCTGCT 60
 Db 353 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGCGCTGCT 412

QY 61 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
 Db 413 TTTGGAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 472

QY 121 GGCATTATCTTCTCGTGGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 180
 Db 473 GGCATTATCTTCTCGTGGGATTTCCAGCAATGCACTAGTAGTATCCACTTACATTTTC 532

QY 181 AAATGAGACCTTGGAGAGCAGCAACATATGCTGAACTGGCTGCACAGATCTG 240
 Db 533 AAATGAGACCTTGGAGAGCAGCAACATATGCTGAACTGGCTGCACAGATCTG 592

QY 241 CTCTATCTGACGACCTCCCTTCTGATTTCACTATGCGAGTGGCGAAACTGGATC 300
 Db 593 CTGTATCTGACGACCTCCCTTCTGATTTCACTATGCGAGTGGCGAAACTGGATC 652

QY 301 TTTGGAGATTTGATGTTAAGTTTATCCGCTTCAGCTTCCATTTCACTGATAGCAGC 360
 Db 653 TTTGGAGATTTGATGTTAAGTTTATCCGCTTCAGCTTCCATTTCACTGATAGCAGC 712

QY 361 ATCCTCTTCTCACCCTGTTTACGATCTTCCGCTACTGTGATCATTCACCCAAATGAGC 420
 Db 713 ATCCTCTTCTCACCCTGTTTACGATCTTCCGCTACTGTGATCATTCACCCAAATGAGC 772

QY 421 TGCCTTTTCCATTCACAAACTCGATGTCAGTTGATGCTGCTGTGTTGGATCATTT 480
 Db 773 TGCCTTTTCCATTCACAAACTCGATGTCAGTTGATGCTGCTGTGTTGGATCATTT 832

QY 481 TCACCTGTTAGCTGTCTATTCGGATGACCTTCTTGATCACATCAACCAAGAGCAACAGA 540
 Db 833 TCACCTGTTAGCTGTCTATTCGGATGACCTTCTTGATCACATCAACCAAGAGCAACAGA 592

QY 541 TCAGCTGTCTCGACCTCACTACCTGATGCGAATCAATTAATTAAGTGGTACACCTTA 600
 Db 893 TCAGCTGTCTCGACCTCACTACCTGATGCGAATCAATTAATTAAGTGGTACACCTTA 952

QY 601 ATTTTGACGTGCACTACTTCTTCCCTCCCTGGTGATGATGACATTTGCTATACCAAG 660
 Db 953 ATTTTGACGTGCACTACTTCTTCCCTCCCTGGTGATGATGACATTTGCTATACCAAG 1012

QY 661 ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
 Db 1013 ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 1072

QY 721 AGGCTAACCACTTCTGCTACTCTTCTGCAATTTACGATGTTTATACCTTCCATATCTTG 780
 Db 1073 AGGCTAACCACTTCTGCTACTCTTCTGCAATTTACGATGTTTATACCTTCCATATCTTG 1132

QY 781 AGGTCATTCGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTCAGAAATCAGATC 840

Db 1133 AGGTGCTATTCGATCGAATCTCGCTGCTTTCATCATGATTTCCATTCGATTCAGATC 1192
 QY 841 CATGAACCTTACATCGTTCCTTAGACCAATAGTCTCTGTAACACCTTTGGTAACTGTTA 900
 Db 1193 CATGAACCTTACATCGTTCCTTAGACCAATAGTCTCTGTAACACCTTTGGTAACTGTTA 1252
 QY 901 CTATATGCTGTTGGTTCAGCGAACATTTTCAGCAGGCTCTGCTCAACAGTGGATGCAAA 960
 Db 1253 CTATATGCTGTTGGTTCAGCGAACATTTTCAGCAGGCTCTGCTCAACAGTGGATGCAAA 1312
 QY 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAGTTTACTCAACAAACCCCTTGA 1014
 Db 1313 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAGTTTACTCAACAAACCCCTTGA 1366

RESULT 5
 ABS51678
 ID ABS51678 standard; DNA; 1851 BP.

XX AC ABS51678;
 XX AC
 DT 05-NOV-2002 (first entry)
 XX

DNA encoding human Purinoceptor-like protein.
 Human; NOVX; pathological condition; NOVX-associated disorder;
 Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
 pancreatitis; obesity; diabetes; autoimmune disease; infertility;
 renal artery stenosis; interstitial nephritis; glomerulonephritis;
 polycystic kidney disease; cataract; Alzheimer's disease; cancer;
 acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
 congenital heart defect; scleroderma; endometriosis; haemophilia;
 dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
 multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
 acne; wound; asthma; human disease; calpain; epsin; zinc finger;
 low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;
 serine protease TLSP; mitogen activated protein kinase kinase-2;
 glypican-2 precursor; thymosin beta-10; gene; ds.

XX Homo sapiens.
 OS
 XX
 PN MO200255702-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 26-OCT-2001; 2001WO-US050925.
 XX
 PR 26-OCT-2000; 2000US-0243320P.
 PR 26-OCT-2000; 2000US-0243592P.
 PR 26-OCT-2000; 2000US-0243642P.
 PR 27-OCT-2000; 2000US-0243681P.
 PR 27-OCT-2000; 2000US-0243681P.
 PR 31-OCT-2000; 2000US-0244443P.
 PR 01-NOV-2000; 2000US-0244995P.
 PR 01-NOV-2000; 2000US-0245029P.
 PR 02-NOV-2000; 2000US-0245293P.
 PR 02-NOV-2000; 2000US-0245315P.
 PR 02-NOV-2000; 2000US-0245316P.
 PR 19-JAN-2001; 2001US-0262994P.
 PR 15-FEB-2001; 2001US-0269056P.
 PR 02-MAR-2001; 2001US-0272923P.
 PR 15-MAR-2001; 2001US-0276565P.
 PR 07-SEP-2001; 2001US-0318119P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Gangolli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L;
 PI Vernet CM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;
 PI Malyankar U, Stone D, Millet I, Smithson G, Gunther E, Padigaru M;
 PI Taupier RJ, Anderson D;
 XX WPI; 2002-590673/63.
 DR P-PSDB; ABG70271.

XX Isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing, diagnosing and researching pathological conditions
PT in humans with a NOVX-associated disorders, e.g. cancer, stroke or
PT Alzheimer's disease.
XX
PS Claim 8; Page 32; 236pp; English.
XX
CC The present invention relates to a new polypeptide that comprises any of
CC 17 fully defined sequences of 43-990 amino acids given in the
CC specification. The NOVX polypeptide, nucleic acid and antibody of the
CC invention are useful for treating or preventing a pathological condition
CC in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau
CC syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,
CC diabetes, autoimmune disease, renal artery stenosis, interstitial
CC nephritis, glomerulonephritis, polycystic kidney disease, cataract,
CC Alzheimer's disease, acoustic trauma, cancer, infertility,
CC cardiomyopathies, atherosclerosis, hypertension, congenital heart
CC defects, scleroderma, endometriosis, haemophilia, multiple sclerosis,
CC Parkinson's disease, Huntington's disease, epilepsy, acne, wounds and
CC anxiety, pain, leukaemias, hypothyroidism, psoriasis, cancer, and
CC asthma. They are also useful for the manufacture of a medicament for
CC treating a syndrome associated with a human disease, specifically a NOVX-
CC associated disorder. They may also be useful in therapeutic applications
CC including protein therapy, as small molecule drug targets, as antibody
CC targets, as diagnostic and/or prognostic markers, in gene therapy, as
CC research tools and in tissue regeneration. The present nucleic acid
CC sequence encodes one of the 17 novel proteins of the invention
XX
SQ Sequence 1851 BP; 509 A; 458 C; 341 G; 543 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 6; Length 1851;
Best Local Similarity 100.0%; Pred. No. 2.6e-289;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGATTTCCCGGATTATGAGCTGCT 60
DB 347 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGATTTCCCGGATTATGAGCTGCT 406
QY 61 TTTGGAATGCTGCTGATGAACATCCCACTCAGATGCTACTCTCCCTGTTATTTAT 120
DB 407 TTTGGAATGCTGCTGATGAACATCCCACTCAGATGCTACTCTCCCTGTTATTTAT 466
QY 121 GCAATTTATCTCTCTGCTGGAATTTCCAGGCAATGCTAGTATGATATCCACTTACATTTTC 180
DB 467 GCAATTTATCTCTCTGCTGGAATTTCCAGGCAATGCTAGTATGATATCCACTTACATTTTC 526
QY 181 AAAATGAGACCTTTGGAAGAGCAGCACATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240
DB 527 AAAATGAGACCTTTGGAAGAGCAGCACATCATTTATGCTGAACTGGCCCTGCACAGATCTG 586
QY 241 CTGTATCTGACGAGCTCCCTTCCCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC 300
DB 587 CTGTATCTGACGAGCTCCCTTCCCTGATTCACCTACTATGCGAGTGGCGAAACTGGATC 646
QY 301 TTTGGAGATTTCAATGTTAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
DB 647 TTTGGAGATTTCAATGTTAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 706
QY 361 ATCCCTCTTCTACCTGTTTTCAGATCTTCCGCTACTGTGTATCATTCACCAATGAGC 420
DB 707 ATCCCTCTTCTACCTGTTTTCAGATCTTCCGCTACTGTGTATCATTCACCAATGAGC 766
QY 421 TGCCTTTTCCATTCACAAATCCGATGTCAGTTGTAGCTGTGCTGGTGTGATCATTT 480
DB 767 TGCCTTTTCCATTCACAAATCCGATGTCAGTTGTAGCTGTGCTGGTGTGATCATTT 826
QY 481 TCACCTGTAGCTGTGATTTCCGATGACCTTCTTGATCATCATCAACCAACAGGACCAACAGA 540
DB 827 TCACCTGTAGCTGTGATTTCCGATGACCTTCTTGATCATCATCAACCAACAGGACCAACAGA 886
QY 541 TCAGCTGTCTCGACCTTCACAGTTCCGATGAACTCAATCACTATTAGTGGTACAACTTA 600

DB 887 TCAGCTGTCTCGACCTCCACAGTTCCGATGAACTCAATCACTATTAAAGTGGTACAACTTA 946
QY 601 ATTTTGAAGTCAACTACTTTCTGCTCCCTCCCTTGGTATAGTACACTTTGTTATACACAG 660
DB 947 ATTTTGAAGTCAACTACTTTCTGCTCCCTCCCTTGGTATAGTACACTTTGTTATACACAG 1006
QY 661 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAAGGACAGA 720
DB 1007 ATTATCCACACTCTGACCCATGGAAGTCAAACTGACAGCTGCTTAAAGCAAGGACAGA 1066
QY 721 AGGCTTAACCACTCTGCTACTCTCTGATTTTACGTTATGTTTAACTCCCTTCCATATCTTG 780
DB 1067 AGGCTTAACCACTCTGCTACTCTCTGATTTTACGTTATGTTTAACTCCCTTCCATATCTTG 1126
QY 781 AGGCTTAACCACTCTGCTACTCTCTGATTTTCAATCACTGTTTCAATGAGTCAAGATCAGATC 840
DB 1127 AGGCTTAACCACTCTGCTACTCTCTGATTTTCAATCACTGTTTCAATGAGTCAAGATCAGATC 1186
QY 841 CATGAAGCTTACATGCTTTCTAGACCATAGCTCTGTAACACCTTTGGTAACTGTTA 900
DB 1187 CATGAAGCTTACATGCTTTCTAGACCATAGCTCTGTAACACCTTTGGTAACTGTTA 1246
QY 901 CTATATGCTGCTGCTCAGGCAAACTTTTCAGAGGCTGCTCTCAACAGTGAAGTGCATA 960
DB 1247 CTATATGCTGCTGCTCAGGCAAACTTTTCAGAGGCTGCTCTCAACAGTGAAGTGCATA 1306
QY 961 GTAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAACCAACCTTTGA 1014
DB 1307 GTAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAACCAACCTTTGA 1360
RESULT 6
AAS07948
ID AAS07948 standard; cDNA; 1014 BP.
XX AAS07948;
XX 23-OCT-2001 (first entry)
DE Human cDNA encoding G-protein coupled receptor, hrUP21.
KW Human; G-protein coupled receptor; GPCR; hrUP21; agonist;
KW inverse agonist; lung cancer; ss.
OS Homo sapiens.
FH Key
FT CDS
FT 1..1014
FT /*tag= a
FT /product= "hrUP21"
XX W0200136471-A2.
XX 25-MAY-2001.
XX 16-NOV-2000; 2000WO-US031509.
XX 17-NOV-1999; 99US-0166088P.
XX 17-NOV-1999; 99US-0166099P.
XX 17-NOV-1999; 99US-0166369P.
XX 23-DEC-1999; 99US-0171900P.
XX 23-DEC-1999; 99US-0171901P.
XX 23-DEC-1999; 99US-0171902P.
XX 11-FEB-2000; 2000US-0181749P.
XX 14-MAR-2000; 2000US-0189258P.
XX 14-MAR-2000; 2000US-0189259P.
XX 10-APR-2000; 2000US-0195898P.
XX 10-APR-2000; 2000US-0195899P.
XX 10-APR-2000; 2000US-0196078P.
XX 28-APR-2000; 2000US-0200419P.
XX 12-MAY-2000; 2000US-0203630P.
XX 12-JUN-2000; 2000US-0210741P.
XX 12-JUN-2000; 2000US-0210982P.

XX An isolated p2Y-like receptor polypeptide (HIPHUM 0000037) which can be
 PT used for the identification of agonists and antagonists which may be used
 PT to treat an immune or inflammatory disease.

XX Claim 5; Page 28-29; 35pp; English.

XX The invention relates to an isolated p2Y-like receptor polypeptide
 CC (ABB83818-ABB83819) which is also referred to in the specification as
 CC HIPHUM 0000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates p2Y receptor activity is useful to treat a
 CC subject having a disorder that is responsive to p2Y-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of p2Y-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polymyositis or prostatitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the p2Y-like receptor variant encoding gene
 CC of the invention

XX SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 5.8e-289;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTAGCAATGCTCTGATTTCCCGGATATGCGAGTCT 60
 DB 1 ATGATGAGCCACTAGACTATTAGCAATGCTCTGATTTCCCGGATATGCGAGTCT 60
 QY 61 TTGGAAATGCACTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
 DB 61 TTGGAAATGCACTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
 QY 121 GGCATTATCTCTCGTGGGATTTCCAGCAATGCACTAGTATGATACCACTACATTTTC 180
 DB 121 GGCATTATCTCTCGTGGGATTTCCAGCAATGCACTAGTATGATACCACTACATTTTC 180
 QY 181 AAATGAGACCTTGGAGAGCAGCAGCACCATTATGCTGAACTGGCTGACAGATCTG 240
 DB 181 AAATGAGACCTTGGAGAGCAGCAGCACCATTATGCTGAACTGGCTGACAGATCTG 240
 QY 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300
 DB 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300
 QY 301 TTGAGAGATTGATGTAAGTTTATCCGCTTCCAGTTCCTTCCATTCAGCTGTATAGCAGC 360
 DB 301 TTGAGAGATTGATGTAAGTTTATCCGCTTCCAGTTCCTTCCATTCAGCTGTATAGCAGC 360
 QY 361 ATCCCTTCTCCTCACTGTTTTCAGCATCTCCGCTACTGTGATCATTCACCCCAATGAGC 420
 DB 361 ATCCCTTCTCCTCACTGTTTTCAGCATCTCCGCTACTGTGATCATTCACCCCAATGAGC 420
 QY 421 TGCTTTTCCATTACAAAATCGATGTCAGTGTGAGCTGTGCTGTGTTGATTCATT 480
 DB 421 TGCTTTTCCATTACAAAATCGATGTCAGTGTGAGCTGTGCTGTGTTGATTCATT 480
 QY 481 TCAGTGTGATGTCATTCCGATGACCTTCTGATCAGATCAACCAAGAGCCACAGAGA 540
 DB 481 TCAGTGTGATGTCATTCCGATGACCTTCTGATCAGATCAACCAAGAGCCACAGAGA 540
 QY 541 TCAGCTGTCTCGAGCTCACCAGTTCGGATGAACTCAATPACTATTAAAGTGTGACACCTTA 600
 DB 541 TCAGCTGTCTCGAGCTCACCAGTTCGGATGAACTCAATPACTATTAAAGTGTGACACCTTA 600
 QY 601 ATTTGACTGCAACTACTTTCTGCTCCCTGGTGGTATGATGACACTTTGCTATACCAGC 660

DB 601 ATTTGACTGCAACTACTTTCTGCTCCCTGGTGGTATGATGACACTTTGCTATACCAGC 660
 QY 661 ATTTGACTGCAACTACTTTCTGCTCCCTGGTGGTATGATGACACTTTGCTATACCAGC 720
 DB 661 ATTTGACTGCAACTACTTTCTGCTCCCTGGTGGTATGATGACACTTTGCTATACCAGC 720
 QY 721 AGGCTAACCACTTCTGCTACTCTCTGCAATTTTACGATTTTACCTTCCATATCTTG 780
 DB 721 AGGCTAACCACTTCTGCTACTCTCTGCAATTTTACGATTTTACCTTCCATATCTTG 780
 QY 781 AGGCTAACCACTTCTGCTACTCTCTGCAATTTTACGATTTTACCTTCCATATCTTG 840
 DB 781 AGGCTAACCACTTCTGCTACTCTCTGCAATTTTACGATTTTACCTTCCATATCTTG 840
 QY 841 CATCAAGCTTACATCGTTTCTAGACCACTTACCTGCTCTGAAACACCTTTGGTAACTGTTA 900
 DB 841 CATCAAGCTTACATCGTTTCTAGACCACTTACCTGCTCTGAAACACCTTTGGTAACTGTTA 900
 QY 901 CTATATGTTGGTGGTTCAGCGAACAATTTTCAGCAGAGCTGTCTGCTCAACAGTGGATGAAA 960
 DB 901 CTATATGTTGGTGGTTCAGCGAACAATTTTCAGCAGAGCTGTCTGCTCAACAGTGGATGAAA 960
 QY 961 GTAAAGCGGAGACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
 DB 961 GTAAAGCGGAGACCTTGGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 8
 AAK98323

ID AAK98323 standard; cDNA; 1014 BP.

XX AAK98323;

DT 30-APR-2002 (first entry)

XX Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 signal transduction; human protease; GPCR disorder; gene therapy;
 transgenic animal; gene; ss.

XX Homo sapiens.

Key Location/Qualifiers

CDS 1..1014

/*tag= a

/product= "G-protein coupled receptor"

XX WO200187980-A2.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001WO-US015957.

XX 18-MAY-2000; 2000US-0205196P.

XX 08-AUG-2000; 2000US-00634656.

XX (APPL-) APPLERA CORP.

XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;

XX WPI; 2002-075312/10.

XX P-PSDB; AAO14027.

XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterized by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies.

XX Claim 23; Fig 1; 64pp; English.

XX The present specifically claimed human cDNA sequence (located on

chromosome 13) encodes a purinergic-related G-protein coupled receptor (GPCR) of the invention. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided into five families, family I contains the purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are characterised by their selective responsiveness towards ATP and its analogues, some also respond to UTP. The invention comprises a human G-protein coupled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the invention is useful for: the development/identification of therapeutic proteins; assays designed to quantitatively determine levels of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. GPCR nucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR expression; and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals

Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 5.8e-289;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCAGCTAGCTATTTAGCAATGCTTCTGATTTCCCGATTATGACGTGCT 60
 DB 1 ATGATGAGCAGCTAGCTATTTAGCAATGCTTCTGATTTCCCGATTATGACGTGCT 60

QY 61 TTTGAAATGTCAGTGAAGCAATCCACCTCAGATGCACTACCTCCCTGTTATTTAT 120
 DB 61 TTTGAAATGTCAGTGAAGCAATCCACCTCAGATGCACTACCTCCCTGTTATTTAT 120

QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATGATATCCACTTACATTTTC 180
 DB 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATGATATCCACTTACATTTTC 180

QY 181 AAATGAGACCTTGAAGAGCAGCAGCAATCATTTATGCTGAACTGGCTGCGCTGCACAGATCTG 240
 DB 181 AAATGAGACCTTGAAGAGCAGCAGCAATCATTTATGCTGAACTGGCTGCGCTGCACAGATCTG 240

QY 241 CTGTATCTGACAGCTCCCTTCTGATTTCACTACTATGCGAGTGGGAAACTGGATC 300
 DB 241 CTGTATCTGACAGCTCCCTTCTGATTTCACTACTATGCGAGTGGGAAACTGGATC 300

QY 301 TTTGAGATTTTATGTGTAAGTTTATCCGCTTCAGCTTCCACTTCAACTGTATAGCAGC 360
 DB 301 TTTGAGATTTTATGTGTAAGTTTATCCGCTTCAGCTTCCACTTCAACTGTATAGCAGC 360

QY 361 ATCTCTTCTCAGCTGTTTTCAGATCTTCCGCTACTGTGATCATTTCAACCAATGAGC 420
 DB 361 ATCTCTTCTCAGCTGTTTTCAGATCTTCCGCTACTGTGATCATTTCAACCAATGAGC 420

QY 421 TGCCTTTCCATTCAGAACTCGATGTCAGTGTGAGCTGTGCTGTGATCATTT 480
 DB 421 TGCCTTTCCATTCAGAACTCGATGTCAGTGTGAGCTGTGCTGTGATCATTT 480

QY 481 TCATGCTAGTGTGCTATTCAGATGCTTCTTGATCAGATCAATCAACCAAGACCAACAGA 540
 DB 481 TCATGCTAGTGTGCTATTCAGATGCTTCTTGATCAGATCAATCAACCAAGACCAACAGA 540

QY 541 TCAGCTGTCTGAGCTCACCAGTTCCGATGCACTCAATTAATTAAGTGTGTAACACCTA 600
 DB 541 TCAGCTGTCTGAGCTCACCAGTTCCGATGCACTCAATTAATTAAGTGTGTAACACCTG 600

QY 601 ATTTGACTGCACTACTTCTGCTCCCTGCTGATGATGACACTTTGCTATACACG 660
 DB 601 ATTTGACTGCACTACTTCTGCTCCCTGCTGATGATGACACTTTGCTATACACG 660

QY 661 ATTATCCACACTGTCACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAACGACGA 720
 DB 661 ATTATCCACACTGTCACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAACGACGA 720

QY 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATGTTTTCCTTCCATATCTTG 780
 DB 721 AGGCTAAACCAATCTGCTACTCTCTTGCATTTTACGATGTTTTCCTTCCATATCTTG 780

QY 781 AGGCTCAATTCGATGAAATCTCGCTGCTTTCAATCAGTTGTTTCCATGAGATCAGATC 840
 DB 781 AGGCTCAATTCGATGAAATCTCGCTGCTTTCAATCAGTTGTTTCCATGAGATCAGATC 840

QY 841 CATGAGCTTTACATCGTTTCTAGACCATGAGCTGCTCTGAAACACCTTTGGTACCTGTTA 900
 DB 841 CATGAGCTTTACATCGTTTCTAGACCATGAGCTGCTCTGAAACACCTTTGGTACCTGTTA 900

QY 901 CTATATGTTGTTGTCAGCGACAACTTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 960
 DB 901 CTATATGTTGTTGTCAGCGACAACTTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 960

QY 961 GTAAGCGGAACTCTGAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTTGA 1014
 DB 961 GTAAGCGGAACTCTGAGCAAGCAAAAGAAATAGTTACTCAAAACACCTTTGA 1014

RESULT 9
 ABK11381
 ID ABK11381 standard; DNA; 1014 BP.
 XX
 AC ABK11381;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human DNA encoding P2Y1-like G protein-coupled receptor.
 XX
 KW Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR; infection;
 KW pain; cancer; anorexia; bulimia; asthma; hypotension;
 KW central nervous system disease; acute heart failure; hypertension;
 KW urinary retention; osteoporosis; diabetes; angina pectoris;
 KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 KW benign prostatic hypertrophy; psychosis; neurological disorder;
 KW dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 KW dementia; severe mental retardation; Huntington's disease;
 KW Tourette's syndrome.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "P2Y1-like GPCR"
 XX
 PN WO200214511-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-EP009243.
 XX
 PR 14-AUG-2000; 2000US-0224989P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI; 2002-257607/30.
 XX
 DR P-P8DB; AAU77600.
 XX
 PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can be
 PT regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia.
 XX

PS Claim 1; Fig 5; 118pp; English.

XX The invention relates to a purified human p2Y₁-like G protein-coupled

CC receptor (GPCR) polypeptide and the nucleic acids encoding it (including

CC 5' and 3 sequences, promoters, fragments, variants, or a sequence

CC encoding a protein at least 50% identical to the GPCR). Also included are

CC an expression vector comprising the nucleic acid, a host cell containing

CC the vector and the identification of modulators of the GPCR especially

CC those that reduce the activity of the GPCR. The nucleic acid is useful

CC for detecting a polynucleotide encoding the GPCR in a biological sample.

CC The GPCR and nucleic acid are useful for screening for agents which

CC decrease the activity of the GPCR and for modulators of the GPCR. The

CC modulator or agent useful for modulating the activity of p2Y₁-like G

CC protein-coupled receptor in a disease such as bacterial, fungal,

CC protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma,

CC central nervous system (CNS) disease, acute heart failure, hypotension,

CC hypertension, urinary retention, osteoporosis, diabetes, angina pectoris,

CC myocardial infarction, ulcer, inflammation, allergy, multiple sclerosis,

CC benign prostatic hypertrophy, psychotic and neurological disorders,

CC dyskinesias, HIV virus infection (human immunodeficiency virus), CNS

CC disorders such as Parkinson's disease, anxiety, schizophrenia, manic

CC depression, delirium, dementia, severe mental retardation, Huntington's

CC disease and Tourette's syndrome. The present sequence encodes the p2Y₁-

CC like GPCR of the invention

XX

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;

Best Local Similarity 99.9%; Pred. No. 5.8e-289;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCAGCTAGACTATTAGCAATGCTTCTGATTTCCCGATTAATGACAGTCT 60

DB 1 ATGAATGAGCAGCTAGACTATTAGCAATGCTTCTGATTTCCCGATTAATGACAGTCT 60

QY 61 TTGGAAATTCAGCTGATGAAACATCCATCAAGATGCACTACCTCCCTGTTATTAT 120

DB 61 TTGGAAATTCAGCTGATGAAACATCCATCAAGATGCACTACCTCCCTGTTATTAT 120

QY 121 GGCATTATCTCTCGTGGATTTCCAGGATGAGTATGATATCCACTTACATTTTC 180

DB 121 GGCATTATCTCTCGTGGATTTCCAGGATGAGTATGATATCCACTTACATTTTC 180

QY 181 AAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACCTGGCCTGCACAGATCTG 240

DB 181 AAATGAGACCTTGAAGAGCAGCAGCATTATGCTGAACCTGGCCTGCACAGATCTG 240

QY 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300

DB 241 CTGTATCTGACAGCCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACCTGGATC 300

QY 301 TTGGAGATTTCACTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360

DB 301 TTGGAGATTTCACTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360

QY 361 ATCTCTTCTCCCTACCTGTTTACGATCTTCCGCTACTGTGATCAITTCACCCATGAGC 420

DB 361 ATCTCTTCTCCCTACCTGTTTACGATCTTCCGCTACTGTGATCAITTCACCCATGAGC 420

QY 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGATGCTGCTGTGCTGTGATCATTT 480

DB 421 TGCTTTTCCATTCACAAACTCGATGTCAGTGTGATGCTGCTGTGCTGTGATCATTT 480

QY 481 TCACCTGGTGTGCTGATTCGGATGCTTCTTGTATCAATCAACAGGACCAACAGA 540

DB 481 TCACCTGGTGTGCTGATTCGGATGCTTCTTGTATCAATCAACAGGACCAACAGA 540

QY 541 TCAGCTGTCTCGACCTCAGCTTCCGATGAACTCAATATTAAGTGGTACACCTTA 600

DB 541 TCAGCTGTCTCGACCTCAGCTTCCGATGAACTCAATATTAAGTGGTACACCTTA 600

QY 601 ATTTGACTGCACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACG 660

DB 601 ATTTGACTGCACTACTTCTGCTCCCTTGGTGTGATGACACTTTGCTATACACG 660

DB 661 ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGTGCCTTTAAGCAGAAAGCAGA 720

DB 661 ATTATCCACACTCTGACCCATGCACTGCAAACTGACAGTGCCTTTAAGCAGAAAGCAGA 720

QY 721 AGCTTAACCACTTCTGCTTACTCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG 780

DB 721 AGCTTAACCACTTCTGCTTACTCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG 780

QY 781 AGGTCATTTGGATCGAATCTCGCTCTTCAATCAGTTGTTCCATTGAGATCAGATC 840

DB 781 AGGTCATTTGGATCGAATCTCGCTCTTCAATCAGTTGTTCCATTGAGATCAGATC 840

QY 841 CATGAACCTTACATCGTTTCTAGACCAATAGCTCTCTGAACACCTTTGGTAACTGTTA 900

DB 841 CATGAACCTTACATCGTTTCTAGACCAATAGCTCTCTGAACACCTTTGGTAACTGTTA 900

QY 901 CTATATCTGTTGTCAGCGACAACTTTTACGAGCTCTCTGCTCAACAGTGCAGATGCAAA 960

DB 901 CTATATCTGTTGTCAGCGACAACTTTTACGAGCTCTCTGCTCAACAGTGCAGATGCAAA 960

QY 961 GTAAGCGGAGACCTTGAAGCAAGCAAAATTAAGTTACTCAAAACACCTTTGA 1014

DB 961 GTAAGCGGAGACCTTGAAGCAAGCAAAATTAAGTTACTCAAAACACCTTTGA 1014

RESULT 10

ABZ42876

ID ABZ42876 standard; DNA; 1014 BP.

XX AC ABZ42876;

XX 06-MAR-2003 (first entry)

XX Human GPCR polynucleotide SEQ ID NO 13.

DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

XX Human drug development; gustatory; taste; fragrance; gene; ds.

KW Homo sapiens.

OS WO200216548-A2.

PN 28-FEB-2002.

PD 30-JUL-2001; 2001WO-1B001446.

PF 04-AUG-2000; 2000JP-00237818.

PR 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA Haga T, Takeda S, Mitaku S;

PI WPI; 2002-304118/34.

XX P-PSDB; ABP95602.

DR Database global search for G protein-coupled receptors, proteins and

PT encoded genes for studying in vivo signal transduction mechanism and

PT identifying targets for drug development.

XX Claim 9; SEQ ID NO 13; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled

CC receptor (GPCR) genes (ABZ42876-ABZ43216) and/or GPCR proteins (ABP95596-

CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane

CC domains with 250-1000 amino acid residues to give a gene homologous with

CC a known GPCR gene. The receptor proteins and encoded genes are useful for

CC studying in vivo signal transduction mechanism and identifying targets

CC for drug development e.g. based on olfactory and gustatory receptors in

CC form of agonists and antagonists by screening intrinsic and extrinsic

CC ligands as bitter taste inhibitors, taste enhancers and fragrance

CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 5.8e-289;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGAATGAGCCCTAGACTATTAGCAAAATGCTTCTGATTTCCCGGATATGCGAGCTGCT 60
DB 1 ATGAATGAGCCCTAGACTATTAGCAAAATGCTTCTGATTTCCCGGATATGCGAGCTGCT 60

QY 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
DB 61 TTTGAAATTTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120

QY 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGCGAGTAGTGATATCCACTTACATTTTC 180
DB 121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGCGAGTAGTGATATCCACTTACATTTTC 180

QY 181 AAATGAGACCTTGGAGAGCAGCACATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240
DB 181 AAATGAGACCTTGGAGAGCAGCACATCATTTATGCTGAACCTGGCCTGCACAGATCTG 240

QY 241 CTGTATCTGACCAAGCTCCCTCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTCGATC 300
DB 241 CTGTATCTGACCAAGCTCCCTCTCTCTGATTCACCTACTATGCGAGTGGCGAAACTCGATC 300

QY 301 TTTGAGATTTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAG 360
DB 301 TTTGAGATTTGATGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAG 360

QY 361 ATCCCTCTCTCCTCCTGTTTTCAGCATCTTCGCTACTGTGTATCATTCACCAATGAGC 420
DB 361 ATCCCTCTCTCCTCCTGTTTTCAGCATCTTCGCTACTGTGTATCATTCACCAATGAGC 420

QY 421 TGCTTTTCCATTCACAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTGTGGATCAAT 480
DB 421 TGCTTTTCCATTCACAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTGTGGATCAAT 480

QY 481 TCACCTGTAGCTGTATTCGATGACCTTCTTGATCACAATCAACCAAGAGCCACAGA 540
DB 481 TCACCTGTAGCTGTATTCGATGACCTTCTTGATCACAATCAACCAAGAGCCACAGA 540

QY 541 TCAGCTGTCTGACCTCAGCTCAGCTGCGATGACTCAATACATTTAAGTGGTACACCTA 600
DB 541 TCAGCTGTCTGACCTCAGCTCAGCTGCGATGACTCAATACATTTAAGTGGTACACCTA 600

QY 601 ATTTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACAG 660
DB 601 ATTTTGACTGCAACTACTTTCTGCTCCCTGCTGGTATGATGACACTTTGCTATACAG 660

QY 661 ATTATCCACACTCTGACCACTGATGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720
DB 661 ATTATCCACACTCTGACCACTGATGCAAACTGACAGCTGCTTTAAGCAGAAAGCAGA 720

QY 721 AGGCTAACCATCTCTACTCTCTGCTTTCATTTTACCTTACCTTCCATATCTTTG 780
DB 721 AGGCTAACCATCTCTACTCTCTGCTTTCATTTTACCTTACCTTCCATATCTTTG 780

QY 781 AGGGTCATTCGGATGCAATCTCGCTCTCTCAATCAGTTGTTCCATTCAGAAATCAGATC 840
DB 781 AGGGTCATTCGGATGCAATCTCGCTCTCTCAATCAGTTGTTCCATTCAGAAATCAGATC 840

QY 841 CATGAAGCTTACATGCTTTCTAGACCAATGCTGCTTCAACACCTTTGGTAACCTGTTA 900
DB 841 CATGAAGCTTACATGCTTTCTAGACCAATGCTGCTTCAACACCTTTGGTAACCTGTTA 900

QY 901 CTATATGTTGGTTCAGCAGCAACTTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 960
DB 901 CTATATGTTGGTTCAGCAGCAACTTTTTCAGAGGCTGCTGCTCAACAGTGAAGTCAAA 960
```

```
QY 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAAATAGTTACTCAAAACACCTTGA 1014
DB 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAAATAGTTACTCAAAACACCTTGA 1014
```

RESULT 11

ABZ59170
ID ABZ59170 standard; DNA; 1014 BP.

XX AC ABZ59170;

XX DT 28-APR-2003 (first entry)

XX DE Human TGR164 protein encoding DNA.

XX KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;
anticonvulsant; hypotensive; hepatotropic; dermatological; human;
immunosuppressive; antiinflammatory; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..1014

XX FT /*tag= a

XX FT /product= "TGR164"

XX PN WO2003004678-A2.

XX PD 16-JAN-2003.

XX PF 01-JUL-2002; 2002WO-US020860.

XX PR 03-JUL-2001; 2001US-0302800P.

XX XX (TULA-) TULARIK INC.

XX PI Tian H, Dai K, Chen J, Zhao J, Cutler G;

XX XX WPI; 2003-210368/20.

XX DR P-PSDB; ABP71377.

XX PT New G-protein coupled receptor polypeptides designated TGR2, TGR38,
TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
for treating or preventing e.g. asthma, multiple sclerosis, stroke or
nephrolithiasis.

XX PS Claim 7; Page 60-61; 74pp; English.

XX CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
polynucleotides. The polypeptides can be expressed by standard DNA
recombination methodology. The polypeptides are useful for screening or
identifying modulators of GPCR or signal transduction. The modulators of
signal transduction are useful for treating or preventing TGR-associated
disorders, e.g. asthma, multiple sclerosis or kidney disease. The
polypeptides are useful as targets for diagnosing or treating e.g.
epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
inflammatory dermatoses. The present sequence represents a human TGR164
protein encoding DNA

XX SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;

Query Match 99.8%; Score 1012.4; DB 8; Length 1014;

Best Local Similarity 99.9%; Pred. No. 5.8e-289;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCCTAGACTATTAGCAAAATGCTTCTGATTTCCCGGATATGCGAGCTGCT 60

DB 1 ATGAATGAGCCCTAGACTATTAGCAAAATGCTTCTGATTTCCCGGATATGCGAGCTGCT 60

1 ATGAATGAGCCACTAGACTATTATTAGCAATGCTTCTGATTTCCCGGATTATGACGCTGCT 60
61 TTGGAAATTTGCACTCATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTAT 120
61 TTGGAAATTTGCACTCATGAAACATCCCACTCAAGATGACACTACCTCCCTGTTATTTAT 120
121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTAGTATGATATCCCACTTACATTTTC 180
121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTAGTATGATATCCCACTTACATTTTC 180
181 AAAATGAGACTTTGGAAGAGCAGCAGCATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240
181 AAAATGAGACTTTGGAAGAGCAGCAGCATCATTTATGCTGAACTGGCCCTGCACAGATCTG 240
241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300
241 CTGTATCTGACGAGCTCCCTTCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300
301 TTGGAGATTTTCACTGTTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
301 TTGGAGATTTTCACTGTTAAGTTTATCCGCTTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
361 ATCCCTTCTTCCCTGTTTTCAGCATCTTCGCTACTGTTGATGATCATTCACCAATGAGC 420
361 ATCCCTTCTTCCCTGTTTTCAGCATCTTCGCTACTGTTGATGATCATTCACCAATGAGC 420
421 TGCTTTTCCATTTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480
421 TGCTTTTCCATTTCAAAAACCTCGATGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 480
481 TCACCTGTTAGTGTTCATTCGATGACCTTCTTTCATCATCACTCAACCAAGCAACAGCA 540
481 TCACCTGTTAGTGTTCATTCGATGACCTTCTTTCATCATCACTCAACCAAGCAACAGCA 540
541 TCAGCTGTCTGACCTTCACTGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 600
541 TCAGCTGTCTGACCTTCACTGTCAGTTGTAGCTGTGCTGTGTTGGATCATTT 600
601 ATTTTGACTGCAACTTCTTTCGCTCCCTTGGTATGATGACACTTTGCTATACCG 660
601 ATTTTGACTGCAACTTCTTTCGCTCCCTTGGTATGATGACACTTTGCTATACCG 660
661 ATTTTGACTGCAACTTCTTTCGCTCCCTTGGTATGATGACACTTTGCTATACCG 720
661 ATTTTGACTGCAACTTCTTTCGCTCCCTTGGTATGATGACACTTTGCTATACCG 720
721 AGGCTTAACATTTCTGCTACTCTTTCGATTTTACGTTATGTTTACCTTCCATATCTTG 780
721 AGGCTTAACATTTCTGCTACTCTTTCGATTTTACGTTATGTTTACCTTCCATATCTTG 780
781 AGGCTTAACATTTCTGCTACTCTTTCGATTTTACGTTATGTTTACCTTCCATATCTTG 840
781 AGGCTTAACATTTCTGCTACTCTTTCGATTTTACGTTATGTTTACCTTCCATATCTTG 840
841 CATGAAGCTTACATCTTTTCTAGCACTTTCGCTTTCGCAACCTTTTGGTAACTGTTA 900
841 CATGAAGCTTACATCTTTTCTAGCACTTTCGCTTTCGCAACCTTTTGGTAACTGTTA 900
901 CTATATGTTGTTGTCAGGACAACTTTTCAGAGGCTGTTCTGCTCAACAGTGAAGTGA 960
901 CTATATGTTGTTGTCAGGACAACTTTTCAGAGGCTGTTCTGCTCAACAGTGAAGTGA 960
961 GTAAGCGGGAACCTTGAGCAACAAAGAAATTTAGTTACTCAACAACTTGA 1014
961 GTAAGCGGGAACCTTGAGCAACAAAGAAATTTAGTTACTCAACAACTTGA 1014

RESULT 13
ID ADC25997 standard; DNA; 1014 BP.
XX
AC ADC25997;
XX

DT 18-DEC-2003 (first entry)
XX Human purinergic receptor P2Y-related GPCRxl0 DNA.
DE virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
XX anorectic; cardiant; hypotensive; osteopathic; antianginal;
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW neurotropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW human; GPCRxl0; purinergic receptor P2Y; ds; gene; chromosome 13.
XX Homo sapiens.
XX
FH Location/Qualifiers
CDS 1..1014
FT /*tag= a
FT /product= "Human purinergic receptor P2Y-related GPCRxl0
FT protein - both "original" and "alternative" versions"
FT /transl_except= (pos:214..216, aa:Asn)
FT /transl_except= (pos:289..291, aa:Asx)
FT /transl_except= (pos:694..696, aa:Cys)
FT /note= "All translation exceptions are present within the
FT "original" protein CDS"
XX
PN US200308080-A1.
XX
PD 08-MAY-2003.
XX
PF 21-JUN-2001; 2001US-00895453.
XX
PR 20-JUN-2000; 2000US-0212908P.
PR 05-DEC-2000; 2000EP-00870289.
XX
PA (COMM/) COMMUNI D.
PA (LANN/) LANNY V.
PA (GOVA/) GOVAERTS C.
PA (PARM/) PARMENTIER M.
PA (DETH/) DETHEUX M.
XX
PI Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;
XX WPI; 2003-657983/62.
XX P-PSDB; ADC25998, ADC26010.
XX
PT New human G-protein coupled receptor, useful for treating receptor-
PT mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
PT acute heart failure, osteoporosis, stroke, ulcer, allergy, or
PT neurological disorders.
XX
PS Claim 18; Page 14-15; 24pp; English.
XX
CC The invention relates to a novel G-protein coupled receptor (GPCR). The
CC receptor, polynucleotide, agonist, reverse agonist and antagonist of the
CC invention may be useful for treating receptor-mediated disorders
CC including viral, fungal or bacterial infections, immune-related disorders
CC such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
CC hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
CC ulcer and allergy, as well as psychotic and neurological disorders such
CC as schizophrenia and dementia, degenerative diseases such as Parkinson's
CC disease and Alzheimer's disease and dyskinesias such as Huntington's
CC disease. The current sequence is that of the human purinergic receptor
CC P2Y-related GPCRxl0 DNA of the invention which is located on chromosome
CC 13.
XX
SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;
Query Match 99.8%; Score 1012.4; DB 10; Length 1014;
Best Local Similarity 99.9%; Pred. No. 5,8e-289;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 301 TTTGGAGATTTCATGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
 Db 301 TTTGGAGATTTCATGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
 QY 361 ATCCTCTTCCTCACCCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTCACCAATGAGC 420
 Db 361 ATCCTCTTCCTCACCCTGTTTCAGCATCTTCGGCTACTGTGTGATCATTCACCAATGAGC 420
 QY 421 TGCTTTTCCATTACAAAATCCGATGTCAGTTGTAGCCCTGCTGTGGTGTGATCATTT 480
 Db 421 TGCTTTTCCATTACAAAATCCGATGTCAGTTGTAGCCCTGCTGTGGTGTGATCATTT 480
 QY 481 TCACTGGTACTGTCTCATTCGGATGACCTTCTTGATCACATCAACCAACAGCAACAGCA 540
 Db 481 TCACTGGTACTGTCTCATTCGGATGACCTTCTTGATCACATCAACCAACAGCAACAGCA 540
 QY 541 TCAGCTGTCTGACCTCACCAGTTCCGATGAACTCAATCACTAATTAAGTGGTACACCTTA 600
 Db 541 TCAGCTGTCTGACCTCACCAGTTCCGATGAACTCAATCACTAATTAAGTGGTACACCTTA 600
 QY 601 ATTTGACTGCAACTACTTTCTGCTCCCTCCCTGCTGATAGTACACTTTGCTATACCAAG 660
 Db 601 ATTTGACTGCAACTACTTTCTGCTCCCTCCCTGCTGATAGTACACTTTGCTATACCAAG 660
 QY 661 ATTATCCACACTCTGACCCATGGAATGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGCA 720
 Db 661 ATTATCCACACTCTGACCCATGGAATGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGCA 720
 QY 721 AGCTAAACCAATCTGCTACTCTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
 Db 721 AGCTAAACCAATCTGCTACTCTCTTGCATTTTACGTATGTTTACCTTCCATATCTTG 780
 QY 781 AGGGTCATTGCGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTCAGATCAGATC 840
 Db 781 AGGGTCATTGCGATCGAATCTCGCTGCTTCAATCAGTTGTTCCATTCAGATCAGATC 840
 QY 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
 Db 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGCTGCTCTGAACACCTTTGGTAACTGTTA 900
 QY 901 CTATATGCTGCTGACGACAACTTTTCAGCAGCTGCTGCTCAACAGTGAATGCAAA 960
 Db 901 CTATATGCTGCTGACGACAACTTTTCAGCAGCTGCTGCTCAACAGTGAATGCAAA 960
 QY 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014
 Db 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAAAACACCTTTGA 1014

RESULT 15

ID ADL96473 standard; cDNA; 1014 BP.

AC ADL96473;

XX 20-MAY-2004 (first entry)

DE Human G protein-coupled receptor (GPCR) cDNA #14.

KW Human; G protein-coupled receptor; GPCR; gene; ss.

OS Homo sapiens.

PN US2003166148-A1.

PD 04-SEP-2003.

PF 16-DEC-2002; 2002US-00321807.

PR 13-OCT-1998; 98US-00170496.

XX 16-NOV-2000; 2000US-00714008.

PA (CHEN/) CHEN R.
 PA (DANG/) DANG H T.
 PA (LOWI/) LOWITZ K P.
 XX

PI Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI; 2003-898073/82.
 DR P-PSDB; ADL96474.
 XX

XX New G protein-coupled receptor (GPCR), useful for preparing a composition
 PT for identifying compounds as receptors, inverse agonists or partial
 PT agonists having potential applicability as therapeutic agents.
 XX

PS Claim 55; SEQ ID NO 27; 82pp; English.
 XX

CC The invention relates to G protein-coupled receptor (GPCR) polypeptides
 CC and the polynucleotides encoding them. The GPCR polypeptides are useful
 CC for preparing a composition for identifying compounds as receptors,
 CC inverse agonists or partial agonists, having potential applicability as
 CC therapeutic agents. This sequence represents human GPCR cDNA of the
 CC invention.
 XX

XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 U; 0 Other;
 QY

Query Match 99.8%; Score 1012.4; DB 11; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 5 8e-289;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60

Db 1 ATGAATGAGCCACTAGACTATTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60

QY 61 TTTGGAATGTCACATGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120

Db 61 TTTGGAATGTCACATGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120

QY 121 GGCAATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATGATATCCATTACATTTTC 180

Db 121 GGCAATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATGATATCCATTACATTTTC 180

QY 181 AAAATGAGACCTTGGAGAGCAGCACCACCATCATTTATGCTGAACTGGCTGCACAGATCTG 240

Db 181 AAAATGAGACCTTGGAGAGCAGCACCACCATCATTTATGCTGAACTGGCTGCACAGATCTG 240

QY 241 CTGTATCTGACAGCCTCCCTTCCCTGCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300

Db 241 CTGTATCTGACAGCCTCCCTTCCCTGCTGATTTCACTACTATGCGAGTGGCGAAACTGGATC 300

QY 301 TTTGGAGATTTCATGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360

Db 301 TTTGGAGATTTCATGTAAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360

QY 361 ATCTCTTCTCCTCACCCTGTTTCAGCATCTTCGGCTACTGTGATCATTTCAACCAATGAGC 420

Db 361 ATCTCTTCTCCTCACCCTGTTTCAGCATCTTCGGCTACTGTGATCATTTCAACCAATGAGC 420

QY 421 TGCTTTTCCATTACAAAACCTGATGTCAGTTGTAGCTGTGCTGTGGTGTGATCATTT 480

Db 421 TGCTTTTCCATTACAAAACCTGATGTCAGTTGTAGCTGTGCTGTGGTGTGATCATTT 480

QY 481 TCACCTGTGCTGACCTCACCAGTTCCGATGAACTCAATACTATTAAAGTGGTACACCTTA 540

Db 481 TCACCTGTGCTGACCTCACCAGTTCCGATGAACTCAATACTATTAAAGTGGTACACCTTA 540

QY 541 TCAGCTGTCTGACCTCACCAGTTCCGATGAACTCAATACTATTAAAGTGGTACACCTTA 600

Db 541 TCAGCTGTCTGACCTCACCAGTTCCGATGAACTCAATACTATTAAAGTGGTACACCTTA 600

QY 601 ATTTGACTGCAAACTACTTTCTGCTCCCTCCCTGCTGATGATGACACTTTGCTATACCAAG 660

Db 601 ATTTGACTGCAAACTACTTTCTGCTCCCTCCCTGCTGATGATGACACTTTGCTATACCAAG 660

QY 661 ATTATCCACACTCTGACCCATGGAATGCAAACTGACACTGCTTAAAGCAAGAACAGCA 720

Tue Nov 2 12:38:24 2004

us-10-763-854-1.rng

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Db 661 ATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTTAAGCAGAAAGCACGA 720
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Db 721 AGGCTAACCAATCTGCTACTCTGCTTGCATTTTACGTATGTTTTTACCCCTTCCATATCTTG 780
Qy 781 AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTGAGAAATCAGATC 840
Db 781 AGGTCATTCGGATCGAATCTCGCTGCTTTCAATCAGTTGTTCCATTGAGAAATCAGATC 840
Qy 841 CATGAAGCTTACATCGTTTCTAGACCAATTAGTCTGCTCTGAACACCTTTGGTAACCTGTTA 900
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Search completed: November 1, 2004, 19:18:48
Job time : 590 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 16:40:57 ; Search time 4520 Seconds
(without alignments)
10608.795 Million cell updates/sec

Title: US-10-763-854-1

Perfect score: 1014

Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb_om:*

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1014	100.0	1014	6	AX305130 Sequence
3	1014	100.0	1014	6	AX464561 Sequence
4	1014	100.0	1014	6	AX675828 Sequence
5	1014	100.0	1014	6	AX661905 Sequence
6	1012.4	99.8	1014	6	CQ798086 Sequence
7	1012.4	99.8	1014	6	AX148186 Sequence
8	1012.4	99.8	1014	6	AX379468 Sequence
9	1012.4	99.8	1014	6	AX384211 Sequence
10	1012.4	99.8	1014	6	AX549361 Sequence
11	1012.4	99.8	1014	6	AX593341 Sequence
12	1012.4	99.8	1014	6	BD144282 Novel G-p
13	1012.4	99.8	1014	9	AB083598 Homo sapi
14	1012.4	99.8	1014	9	AF411109 Homo sapi
15	1012.4	99.8	1029	6	AX593346 Sequence
16	1012.4	99.8	1081	6	AX458238 Sequence
17	1012.4	99.8	1092	9	AF370886 Homo sapi
18	1012.4	99.8	1179	6	AX593351 Sequence
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22	1012.4	99.8	2285	6	CQ843336 Sequence
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39	735.6	72.5	1014	6	CQ798088 Sequence
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ALIGNMENTS

RESULT 1	BD187507	BD187507	1014 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD187507	Novel Polypeptide.				
DEFINITION	BD187507	Novel Polypeptide.				
ACCESSION	BD187507.1	GI:32997246				
VERSION	BD187507.1	GI:32997246				
KEYWORDS	JP 2003024081-A/1.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1014)				
AUTHORS	Fidock M.D.					
TITLE	Novel Polypeptide					
JOURNAL	Patent: JP 2003024081-A 1 28-JAN-2003;					
COMMENT	Pfizer Ltd (EP/GB) only, Pfizer Inc (US JP EP except GB)					
	OS Homo sapiens					
	PN JP 2003024081-A/1					
	PD 28-JAN-2003					
	PF 17-DEC-2001 JP 2001382712					
	PR 18-DEC-2000 GB 0030854.4, 04-MAY-2001 GB 0111031.1 PI					
	mark david fidock					
	CC					

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/mol_type="genomic DNA"	
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Db	1	ATGAATGAGCCACTAGACTATTATAGCAATGCTTCTGATTTCCCGATTATGACGTGCT 60		
QY	61	TTTGGAAATTGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTAT 120		
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LOCUS      AX464561
DEFINITION Sequence 1 from Patent EP1219638.
ACCESSION AX464561
VERSION    AX464561.1 GI:21899357
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Fiddock,M.D.
TITLE      G-protein coupled receptors having homology to the p2y
JOURNAL    Patent: EP 1219638-A 1 03-JUL-2002;
Pfizer Limited (GB); Pfizer Inc. (US)
FEATURES   Location/Qualifiers
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Query Match 100.0%; Score 1014; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.8e-257;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS      AX675828
DEFINITION Sequence 5 from Patent WO02057452.
ACCESSION AX675828
VERSION    AX675828.1 GI:29333662
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shinkets,R.A., Colman,S.D., Spytek,K.A., Ballinger,R.A., Guo,X.,
Tchernev,V.T., Shenoy,S.G., Li,L., Ellerman,K.E., Zerhusen,B.D.,
Patturajan,M., Casman,S.J., Boldog,F., Gusev,V.Y., Burgess,C.E.,
Edinger,S., Gangolli,E.A., Malyankar,U.M., Gunther,B., Smithson,G.,
Millett,I. and Gerlach,V.L.
TITLE      Human proteins, polynucleotides encoding them and methods of using
JOURNAL    Patent: WO 02057452-A 5 25-JUL-2002;
Curagen Corporation (US)
FEATURES   Location/Qualifiers
source     1..1560
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Query Match 100.0%; Score 1014; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 2.9e-257;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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LOCUS
DEFINITION Sequence 7 from Patent WO02055702.
ACCESSION AX661905

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VERSION AX661905.1 GI:29162960  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Gangoli, E.A., Spytek, K.A., Gilbert, J., Casman, S., Blalock, A.,  
Li, L., Vernet, C.A., Shenoy, S., Mishra, V., Furtak, K., Gerlach, V.,  
Edinger, S., Malvankar, U., Stone, D., Millet, I., Smithson, G.,  
Gunther, E., Padigaru, M., Taupier, R.J., and Anderson, D.  
TITLE Human proteins, polynucleotides encoding them and methods of using  
the same  
JOURNAL Patent: WO 02055702-A 7 18-JUL-2002;  
Curagen Corporation (US)  
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Best Local Similarity 100.0%; Pred. No. 2.9e-257;  
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION Sequence 1 from Patent WO2004029626.
ACCESSION  CQ798086
VERSION    CQ798086.1 GI:46426507
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Inbe, H. and Encinas, J.
TITLE      Regulation of human p2y15 G protein-coupled receptor
JOURNAL    Patent: WO 2004029626-A 1 08-APR-2004;
            Bayer HealthCare AG (DE)
FEATURES   Location/Qualifiers
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CDS
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Query Match      99.8%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 27 from Patent WO0136471.
ACCESSION  AXI48186
VERSION    AXI48186.1 GI:14347086
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE  1
AUTHORS    Chen, R., Dang, H. T. and Lowitz, K. P.
TITLE      Endogenous and non-endogenous versions of human G protein-coupled
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JOURNAL    Patent: WO 0136471-A 27 25-MAY-2001;

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Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS Sequence 2 from Patent WO0208183.
DEFINITION AX593341
ACCESSION AX593341
VERSION AX593341.1 GI:28374719
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Carlton, M., Aparicio, S., Dixon, J. and Hendrick, A.
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DEFINITION Novel G-protein coupled receptors.

BD144282
ACCESSION

BD144282.1 GI:27850040

VERSION JP 2002112793-A/7.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PN

PD

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PI

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C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K45/00, PC

A61K48/00,

PC

A61P43/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC

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AB083598

LOCUS

AB083598 1014 bp DNA linear PRI 24-MAY-2002

DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor, complete CDS, clone:hGPCR16.

ACCESSION AB083598

VERSION AB083598.1 GI:20152259

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.

TITLE Identification of G protein-coupled receptor genes from the human genome sequence

JOURNAL Unpublished

AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.

TITLE Direct Submission

JOURNAL Submitted (10-APR-2002) Shigeki Takeda, Gunma University, Department of Biological and Chemical, Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:stakeda@bce.gunma-u.ac.jp, Tel:++81-277-30-1434, Fax:++81-277-30-1434)

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Location/Qualifiers

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DEFINITION AF411109

ACCESSION AF411109

VERSION AF411109.1 GI:16566322

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

TITLE Discovery and mapping of ten novel G protein-coupled receptor genes

JOURNAL Gene 275 (1), 83-91 (2001)

MEDLINE 21458557

PUBMED 11574155

REFERENCE 2 (bases 1 to 1014)

AUTHORS Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

TITLE Direct Submission

JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. 4953, Toronto, Ont M5S 1A8, Canada

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Location/Qualifiers

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Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Sequence 7 from Patent WO2008183.
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VERSION AX593346.1 GI:28374721
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SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Carlton,M., Aparicio,S., Dixon,J. and Hendrick,A.
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Best Local Similarity 99.9%; Pred. No. 7.4e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Perfect score: 1014

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Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb_est3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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genomic survey sequence.
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VERSION
GSS.
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SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
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AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1014)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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AY404080

VERSION AY404080.1 GI:39760063
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1005)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1005)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..1005
/organism="Pan troglodytes"
/mol_type="genomic DNA"
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Best Local Similarity 94.2%; Pred. No. 2.9e-261;
Matches 947; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 10 CCACCTAGACTATTAGCAAAATGCTTCTGATTTCCCGGATTATGACAGTCTCTTTTGGAAAT 69
Db 1 CCACCTAGACTATTAGCANNNNTTCTGATTTCCCGGATTATGACAGTCTCTTTTGGAAAT 60
Qy 70 TGCACCTGATGAAACATCCCACTCAAGATGACATCACTCCCTGTTTATTTATGGCAATTC 129
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Qy 130 TTCTCTGCGGATTTCCAGGCAATGACAGTAGTGATATCCACTTACATTTTCAAAATGAGA 189
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Qy 190 CTTTGGAAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCACAGATCTGCTGTATCTG 249
Db 181 CTTTGGAAAGAGCAGCACCACATCATTTATGCTGAACCTGGCTGCACAGATCTGCTGTATCTG 240
Qy 250 ACCAGCTCCCTTCCCTGATTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
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Qy 430 ATTCAAAAACCTGAGTGCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
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Qy 490 GCTGTCTTCCGATGACCTTCTTGTATCATCAACCAAGAGCAACCAAGAGATCAGCTCT 549


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Db      961 GCACGGGGGACCTTGACAAAGGAAGAAAGACAGTTGCTCAACACACCCCTTGA 1014

RESULT 4
CC579146      870 bp      DNA      linear      GSS 18-JUN-2003
LOCUS      CH240_458M22.T7 CHORI-240 Bos taurus genomic clone CH240_458M22,
DEFINITION      genomic survey sequence.
ACCESSION      CC579146
VERSION      CC579146.1 GI:31924524
KEYWORDS      GSS.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
REFERENCE      1 (bases 1 to 870)
AUTHORS      Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
      Tsai,M., Cloutier,A., Lee,D., Girm,N., Olson,T., Mayo,M.,
      Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
      Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
      Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
      Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
      Unpublished (2003)
      Other GSSs: CH240_458M22.TARBAC13P2
      Contact: Rob Holt
      Sequencing
      The British Columbia Cancer Agency Genome Science Centre
      600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
      Tel: 604-677-6085
      Fax: 604-877-6276
      Email: rholt@bcgsc.ca
      Clones are derived from the bovine BAC library CHORI-240
      (http://www.chori.org/bacpac/bovine240.htm). For BAC library
      availability, please contact Pieter de Jong (pjejong@mail.cho.org).
      Clones may be purchased from BACPAC Resources
      (http://www.chori.org/bacpac/ordering/information.htm). This work
      was undertaken as part of the International Bovine BAC Mapping
      Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
      British Columbia Genome Sciences Centre, Canada.
      Plate: 458 row: M column: 22
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      Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
      library (Male) produced by Pieter de Jong"

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      Query Match      37.6%; Score 381.6; DB 9; Length 870;
      Best Local Similarity      84.8%; Pred. No. 1.3e-98;
      Matches 451; Conservative      0; Mismatches 79; Indels 2; Gaps 2;

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      1 ATGATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGGATTATG-CAGCTGC 59
      339 ATGATGAGCCACTAGATGATTTTGCNAATGCTCTGATTTCCCTGATTATGTCAGCTGC 398
      60 TTTTGGAAATTCATCGATGAAACATCCCATCAAGATGCACCTACCTCCCTGTTATTTA 119
      399 TCTTGAAATTCACCAAGTGAATAATCCCATCAAGAGCGCACTACCTCCCTGTTATTTA 458
      120 TGGCATTA-TCTTCTCGGGGATTTCCAGGCAAGTCAGTAGTATGCCACTTACATTT 178
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Qy      359 GCATCTCTTCTCCTACCTGTTTTCAGCATCTTCGCTACTGTGTGATCAATTCACCAATGA 418
      699 GCATCTCTTCTCCTACCTGTTTTCAGCATCTTCGCTACTTTCGCTACTTTCATTCACCCACGA 758

Qy      419 CTGTCTTTTTCATTCACAAACTCGATGTCAGTTGTCAGTTGTCAGTGTGCTGTGTGGATCA 478
      759 GCTGCTTCTCCGTCACAAAGAGATGGGCGCATGGTGGCTGTGTGTGTGGATCG 818

Qy      479 TTTCACTGTGTAGTGTCTATTCGATGACCTTCTTTGATCAGATCAACCAACAG 530
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RESULT 5
BM723768      744 bp      mRNA      linear      EST 01-MAR-2002
LOCUS      UI-E-E01-aix-g-16-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
DEFINITION      UI-E-E01-aix-g-16-0-UI 5', mRNA sequence.
ACCESSION      BM723768
VERSION      BM723768.1 GI:19045099
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 744)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
      Normalization and subtraction: two approaches to facilitate gene
      discovery
      Genome Res. 6 (9), 791-806 (1996)
      97044477
      8889548
      Contact: Soares, MB
      Coordinated Laboratory for Computational Genomics
      University of Iowa
      375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
      Tel: 319 335 8250
      Fax: 319 335 9565
      Email: bento-soares@uiowa.edu
      Tissue Procurement: Dr. Gregg Hageman
      cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: Researchers may obtain clones from Research
      Genetics (www.resgen.com).
      Seq primer: M13 Reverse.
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          /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
      modified polylinker; Site 1: EcoR I; Site 2: Not I;
      UI-E-E01 is a normalized cDNA library containing the
      following tissue(s): fetal eye. The library was

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constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 24.0%; Score 243; DB 4; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.4e-58; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 772 CATATCTTTGAGGTCATTGGATCGAATCTCGCTGCTTTCATCAGTTGTTCCATTGAG 831
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QY 832 AATCAGATCCATGAGCTTACATGCTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGT 891
Db |||||
61 AATCAGATCCATGAGCTTACATGCTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGT 120
QY 892 AACCTGTTACTATATGTTGGTGTGAGGACAACTTTTCAGAGCGCTGTCTGCTCAACAGTG 951
Db |||||
121 AACCTGTTACTATATGTTGGTGTGAGGACAACTTTTCAGAGCGCTGTCTGCTCAACAGTG 180
QY 952 AGATGCAAGTAAGCGGAACTTTCAGCAAGCAAGAAATTTAGTTACTCAACAAACCTT 1011
Db |||||
181 AGATGCAAGTAAGCGGAACTTTCAGCAAGCAAGAAATTTAGTTACTCAACAAACCTT 240
QY 1012 TGA 1014
Db |||||
241 TGA 243

RESULT 6

CN511791
LOCUS CN511791
DEFINITION AGENCOURT_22438125 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7269123
5', mRNA sequence.
ACCESSION CN511791
VERSION CN511791.1 GI:46824415
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 800)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabp-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM15249 row: j column: 01
High quality sequence stop: 713.
Location/Qualifiers
1..800
/organism="Danio rerio"

FEATURES

source

ORIGIN

Query Match 18.7%; Score 189.6; DB 7; Length 800;
Best Local Similarity 54.6%; Pred. No. 3.7e-43;
Matches 400; Conservative 0; Mismatches 330; Indels 3; Gaps 1;
QY 57 TGCTTTTGGAAATTCGACTGATGAAAAATCCCACTCAAGATGCACCTACCTCCCTGTAT 116
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70 TTCTTTTGACAACCTGACCGGATGTGGAGCAAGAGTGAAGCGCTACTATCTGCCAGCCAT 129
QY 117 TTATGGCAATATCTCTCGTGGGATTTCCAGGCAATGCAGTAGTGATCCACTTACAT 176
Db |||||
130 GTACGGTGCCATCTTCATAGTGGGTGATTTGGAACAATCACAGCTCTTCGTGTATCT 189
QY 177 TTTCAAAATGAGACCTTTGGAAGAGCAGCACCACCATCATTTATGCTGAACTGGCGTCACAGA 236
Db |||||
190 GCTCAAGGTTGACCTTGGAGAGCAGCACCACCATCATCTGTTGAACCTGGTCTCACAGA 249
QY 237 TCTGCTGTATCTGACAGCCTCCCTTCCTGATTCACCTACTACTATGCGAGTGGCGAAACTG 296
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250 TCTCCTCTTCATGATCTCGCTGCCATTTTATGTTAGTTACTATGTTGCTGAATGACTCGTG 309
QY 297 GATCTTTGGAGATTCATGTGTAGTTTATCGCTTCAGCTTCCATTTCAACCTGTATAG 356
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310 GACTCTGGGAATACCGTGTGCGCTTCGCGGCTTCATCTTCCACTTCAACCTGTACGG 369
QY 357 CAGCATCTCTTCCTCACCTGTTTCAGCATCTTCGCTACTGTGTGATCATTCACCCAT 416
Db |||||
370 CAGCATCTCTTCCTCACATGCTTCTCATTTTTCGCTATGTAGCAATCGTGCATCCGA 429
QY 417 GAGCTGCTTTTCCATTCACAAACTTCGATGTGCACTGTAGCTGTGTGTGTGTGTGTGT 476
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430 GCACCTCACACAAGATTTCGGCGCAACGCTGGGGCGTTGTATCTTGTGCGCTGTGTGTGT 489
QY 477 CATTTTCATCTGT 536
Db |||||
490 TGTACAGTGGCTGAACCTGAGTGCACATTTTAACTGTTTTCGCGATGGAGATCGATAA 549
QY 537 CAGATCAGCTGTCTCGACCTCACAGTTCGGATGAACTCAATACTATTAAAGTGTGTACAA 596
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550 CAAACATCTGTTGGATTTTGGAGCAATGATGCTC---AAAAGATTTGGCGGTATAG 606
QY 597 CCTAATTTTGTGCAACTACTTTCTGCTCCCTTGGGTGTGTGTGTGTGTGTGTGTGTGTGT 656
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607 TTGGGTGTGACAGTACTTGGCTATTTAGTTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGT 666
QY 657 CACGATATCCCACTCTGACCCATGAGTCAAACTGACAGCTGCCTTAAAGCAGAAAGC 716
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667 GCGCATCATCAAAAGCTTAAAGAGGGTCTCATATGCGGTGGCNAAAACGAGTGCAGC 726
QY 717 ACGAAGGTAACCACTCTGCTACTCTTCTGCTATTTTACGTATGTTTTCACCTTCCATAT 776
Db |||||
727 GAGGAGATTCATGCTGCTCATTTTTCAGCTGTTTTCGCGTGTGTGTGTGTGTGTGTGTGT 786
QY 777 CTTGAGGTCATT 789
Db |||||
787 GCTGCGAGCGTTT 799

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Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC10). Library was constructed by Open Biosystems (Huntsville, AL)"

Db	Qy	Df
CA385979	667487	NCCOWA 1RT Oncorhynchus mykiss cdna clone lrt136006_c_h03
CA385979	667487	5', mRNA sequence.
CA385979	667487	GI:24712978
Oncorhynchus mykiss (rainbow trout)		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
1 (bases 1 to 725)		
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,		
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.		
Sequence analysis of a rainbow trout cdna library and creation of a		
gene index		
Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)		
Contact: Rexroad CE		
USDA, ARS, National Center for Cool and Cold Water Aquaculture		
11876 Leetown Road, Kearneysville, WV 25430, USA		
Tel: 304 724 8340 x2129		
Fax: 304 725 0351		
Email: crexroad@nccwa.ars.usda.gov		
Single pass sequencing. Bases called with phred v0.020425.c and		
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cross match v0.990329.		
Seq primer: AGCGGATAACAATTTTCACAGGA.		
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/clone_lib="NCCOWA 1RT"		
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Library made from pooled tissue from brain, gill, liver,		
spleen, muscle, and kidney."		
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Query Match	18.3%;	Score 185.8; DB 6; Length 725;
Best Local Similarity	55.4%;	Pred. No. 4.5e-42;
Matches	402;	Conservative 0; Mismatches 317; Indels 6; Gaps 2;
Qy	218	TGAACCTGGCGCTGCACAGATCTGTATCTGACCAGCCTCCCTTCTGATCTACTACT 277
Df	2	TCAAACCTGGCGTTGACGGATCTTCTGTATGTTCTGATCTGCTTTCATGGTCTACTACT 61
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Df	62	ACACCAACGGTGAATCTCTGAGCGGCGGACCTTCATGTTGCTGCTTTCGCTTTCGGGT 121
Qy	338	TCAATTTCAACCTGTATAGCAGATCTCTTCTGACCTGTTTCAGCATCTTCGCTACT 397
Df	122	TCCAATTTAACCTATATGATAGTATCTGTTCTCACCTGTTTGGCTGTGTTTCGATATG 181
Qy	398	GTTGGATCATTTACCCCAATGAGTGTCTTTTCCCATTCACAAAACCTCGATGTCAGTTGTAG 457
Df	182	TGTTGGCGGCGCATCTCTGAGGGCGCGAGGTGACGAGGAGTGGGTATCTTGG 241
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Qy	578	ATACTATTAGTGGTACAACTAATTTTGTGTCGAACACTTTTCTGCCTCCCCCTTGGTGA 637

TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL
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98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

CDS

polyA signal

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Analysis of the mouse transcriptome based on functional annotation
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Nature 420, 563-573 (2002)
6 (bases 1 to 3613)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitho, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
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RESULT 10
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Mus musculus P2RY1 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
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Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1122)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 50.5%; Pred. No. 9.3e-33;
Matches 433; Conservative 0; Mismatches 412; Indels 12; Gaps 2;

QY 82 AACATCCCATCAAGATGACTACCTCCCTGTTATTTATGGCATATCTTCCTCGTGGGA 141
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Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:9130210N15 product:P2Y PURINOCPTOR 1, full insert
sequence.
AK033660
HTC; CAP trapper.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
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Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
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ORIGIN

Query Match 15.2%; Score 153.8; DB 3; Length 2203;
Best Local Similarity 50.5%; Pred. No. 1.2e-32;
Matches 433; Conservative 0; Mismatches 412; Indels 12; Gaps 2;

QY 82 AACATCCCACTCAAGATGACGATCTCCCTGTTTATTATGCGATTATCTTCTCGTGGGA 141
 Db 779 AAGACGGTTTCCAGTCTTACTACCTGCGGCTGTCTACATTTTAGTTTCATCATAGGC 838
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RESULT 12

AK036611
 LOCUS AK036611 3888 bp mRNA linear HTC 03-APR-2004
 DEFINITION Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830141G17 product:P2Y PURINOCEPTOR 1, full insert sequence.

ACCESSION AK036611

VERSION AK036611.1 GI:26331551

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

FEATURES

source

COMMENT

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3888)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1122)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
AUTHORS Direct Submission
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
JOURNAL
COMMENT This sequence was made by sequencing genomic exons and ordering
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CF284315 781 bp mRNA linear EST 14-AUG-2003
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 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 781)

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics

National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cagabs-x@mail.nih.gov
 Tissue Procurement: Dr. Igor Dawid
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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FEATURES

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CA367446
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 EST.
 Oncorhynchus mykiss (rainbow trout)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2004, 14:50:30 ; Search time 43 seconds
(without alignments)
754.071 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	479	27.0	373	2 A47556	ATP receptor P2u -
6	438	24.7	375	2 A54946	P-2U nucleotide re
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9	405	22.9	328	2 JC4800	P2Y6 receptor - hu
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11	396.5	22.4	432	2 A43448	thrombin receptor
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13	388.5	21.9	425	2 A37912	thrombin receptor
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25	348	19.6	354	2 IS3033	interleukin-8 rece
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ALIGNMENTS

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JC4737

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N.Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C.Species: Homo sapiens (man)

C.Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C.Accession: JC4737; JC4615; S54253

R.Janssens, R.; Communi, D.; Piroton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A.Title: Cloning and tissue distribution of the human P2Y1 receptor.

A.Reference number: JC4737; MUID:96205320; PMID:8630005

A.Accession: JC4737

A.Molecule type: DNA

A.Residues: 1-373 <JAN>

A.Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AA847091.1; PID:g183943

R.Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A.Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A.Reference number: JC4615; MUID:96158962; PMID:8579591

A.Accession: JC4615

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A.Cross-references: GB:U42029; NID:gl147730; PIDN:AAA97872.1; PID:gl147731

A.Experimental source: erythro leukemia cells

R.leon, C.; Vial, C.; Cazenave, J.; Gachet, C.

submitted to the EMBL Data Library, May 1995

A.Description: Cloning of a human putative P2Y receptor.

A.Reference number: S54253

A.Accession: S54253

A.Status: Preliminary

A.Molecule type: mRNA

A.Residues: 1-137,139-373 <LEO>

A.Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA9066.1; PID:g798836

C.Comment: This receptor belongs to a family of G protein-coupled receptors. It responds

C.Genetics:

A.Gene: P2Y1; GDB:P2Y1

A.Cross-references: GDB:677125; OMIM:601167

A.Map position: 3pter-3qter

C.Superfamily: ATP receptor P2u

C.Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote

F.52-77/Domain: transmembrane #status predicted <TM1>

F.124-152/Domain: transmembrane #status predicted <TM3>

F.171-191/Domain: transmembrane #status predicted <TM4>

F.214-237/Domain: transmembrane #status predicted <TM5>

F.261-282/Domain: transmembrane #status predicted <TM6>

F.305-328/Domain: transmembrane #status predicted <TM7>

F.11,27,113,197/Binding site: carboxylate (Asn) (covalent) #status predicted

F.258,336/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F.330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F.343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen

Matches	101;	Conservative	64;	Mismatches	119;	Indels	4;	Gaps	2;
---------	------	--------------	-----	------------	------	--------	----	------	----

QY	26	DENIPLKQXHLPVYIGYIFLVPFGCNAVISTYIFQKRPKWSSTIIMLNLA	CTLLVLT	85
Db	30	DED--FKFILLPVGYAVFVLGLGNAPTLWLFRI	LPDPDATATYFHLSTLVL	87
QY	86	LPFLIHYAGSNNWFGDFMCKFIRFSFHNLXSSILFLTCFSIFRYCVIIHPM	SCFSIH	145
Db	88	LPTLIYVYAAHNHWPFGTEICKPVRFLFYWNLYCSVLFLTCISVHRVYLG	ICHPLRALRWG	147
QY	146	KTRCAVACAVWIIISLVAVIPMTFLTISTNRTNRSACLDLTSSDELNTKWN	LILAT	205
Db	148	RPLRAGLLCLAVNLVAVAGCLVPLFFVTTSKGTTLVLTCHDTRDEEFDHY	VHFSSAVWL	207
QY	206	TFCLPLVIVTLCYTTIITHLTHGL--QTDCLKQKARLLTILLARLYVCF	LPHILRVI	263
Db	208	LFGVPCVLTVLCYGLMARRLYQPLFGSAQSSRLSLRTIAVLT	FAVCFVPFHTRTI	267
QY	264	RIESRLTISCSITENQHEAYIVSRPLAALNTFGNLLLYVVSDFNQ	311	
Db	268	YYLARLEADCRVLNIVNVYKVTPLASANSCLDPVLYLLTGDKYR	315	

RESULT	5
A47556	
ATP	Receptor P2u - mouse
C:	Species: Mus musculus (house mouse)
C:	Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:	Accession: A47556
R:	Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
C:	Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:	Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A:	Reference number: A47556; MUID: 93281707; PMID: 7685114
A:	Accession: A47556
A:	Status: preliminary
A:	Molecule type: mRNA
A:	Residues: 1-373 <LUS>
A:	Cross-references: UNIPROT:P35383; GB:L14751; NID:G309457; PIDN:AAA39871.1; PFI
C:	Superfamily: ATP receptor P2u
C:	Keywords: transmembrane protein

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Query Match      27.0%; Score 479; DB 2; Length 373;
Best Local Similarity 34.4%; Pred. No. 2.1e-33;
Matches 97; Conservative 58; Mismatches 117; Indels 10; Gaps 2;

QY      28  NIPKMHYLPVIGIIFLVGFGPNVAVISTYIFKMPKSKSTTIMNLACTDLYLITSLP 87
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      28  NEDFKVLGVSVGVGVCLGLCNLVVALYIFLCRLKLTWNASTTYPFLAVSDSLYAASLP 87
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      88  FLHYIYASGENWIFGDFMCKFIRFSFHNLYSSILFLTCTFSIERVCIITHPMSCFSIHKT 147
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      88  LLVYYYARGDHWFFSVLCKLVRFLEPTNYLCISILFLTCTSVHRCLGVRLPHSLRWGRA 147
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      148  RCVAVCANVWIIISLVAVIPMTLITSTNRTNSACLDITSSDELNTIKWYNLILFATTF 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      148  RYARRVAAVWVVLVLAQAPLVYFVTTSVRGTRITCHDTSARELFHFVAYSSWMLGLLF 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      208  CLPLVAVTLCTYTIIHTEL-----THGLQTDSCLKAKRRLTILLALLAFYVCFLPFHIL 260
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      208  ANPFSVILVCYVLMARRLLKPAYGTGGPLR---AKRKSVRTIALVLAFLCFLPFHVT 264
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      261  RVRIEIRLLISCSISENOIHEAYIVSRPLAALNTFGNLLLY 302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      265  RTLYYSFRSLDSCHTLNAINMAYKITRPLASANSCLDPVLY 306
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
A54946
P-2U nucleotide receptor - human
C:Species: Homo sapiens (man)
C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C/Accession: A54946
R:Parx, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Ols

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Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A>Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic fibrosis therapy.

A|Reference number: A54946; MUID:94211846; PMID:8159738

A|Accession: A54946

A>Status: preliminary

A|Molecule type: mRNA, protein

A|Residues: 1-375 <PAR>

A|Cross-references: GB:U07225

A|Note: parts of this sequence were confirmed by protein sequencing

C|Genetics:

A|Gene: GDB:P2RV2; HP2U; p2U

A|Cross-references: GDB:362713; OMIM:600041

A|Map position: llq13.5-llq14.1

C|Superfamily: ATP receptor P2u

C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.7%; Score 438; DB 2; Length 375;
Best Local Similarity 33.0%; Pred. NO. 6.7e-30;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4;

Qy 28 NIPLKHWYLVPIYGIFLFGPGNAVISTYTFKMPKWSSTIIMLNACTDLDLYLTSLP 87
 | || | || | : || : || : || : || : || : || : || : || : ||
Db 28 NEDFKVLLPVSYGVVVGLGCLNAGVLIFLCRLKTWASTTMYMHLAVSDALYAASLP 87
 | || | || | : || : || : || : || : || : || : || : || : ||

Qy 88 FLIHYYASGENWIIGDFGMCKFRFSHFHNLXSSILFETCFISFYRCVIHPMSCFSIHT 147
 | || | || | : || : || : || : || : || : || : || : || : ||
Db 88 LLVYYARGDHWPFFTVLCKVRFLFYTNLYCSILEFTCI SVHRCLGVRPLRSRWGRA 147
 | || | || | : || : || : || : || : || : || : || : || : ||

Qy 148 RCADVACAAVMILI SAVIPMTFLTITSTNRKSACLDTSSDELNTIKWNLI L TATTF 207
 | || | || | : || : || : || : || : || : || : || : || : ||
Db 148 RYARRVAGAVWLVLJACQAPVLIVFTTSAR - GLPTCHDTSAPELFSRFVAYSSVMGLLF 206
 | || | || | : || : || : || : || : || : || : || : || : ||

Qy 208 CLPLIVVTLCYTII I HTL-----THGIQTDSCLKOKARRLTILLILA FVCVCPFHIL 260
 | || | || | : || : || : || : || : || : || : || : || : ||
Db 207 AVPEAVILCVVLMARLLKPAYSGGPLR--AKRKSVRTIAVLVAVALCFLPHVT 263
 | || | || | : || : || : || : || : || : || : || : || : ||

Qy 261 RVIRIESRLSISCIENIQIEHYIVSRPLAINTFNGLLY 302
 | || | || | : || : || : || : || : || : || : || : || : ||
Db 264 RTLYYSFRSLDSLCHTLNAINMAKVTR-LASANSCLDPVLY 304
 | || | || | : || : || : || : || : || : || : || : || : ||

RESULT 7

I55450

G protein-coupled P2 receptor - rat

C|Species: Rattus norvegicus (Norway rat)

C|Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C|Accession: I55450

R|Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995

A>Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.

A|Reference number: I55450; MUID:96064682; PMID:7592819

A|Accession: I55450

A>Status: preliminary;

A|Molecule type: mRNA

A|Residues: 1-328 <RES>

A|Cross-references: UNIPROT_Q63371; GB:D63665; NID:g1066007; PID:BAAA09816.1; PID:g1066007

C|Superfamily: ATP receptor P2u

C|Keywords: G protein-coupled receptor

Query Match	23.9%;	Score 423;	DB 2;	Length 328;
Best Local Similarity	32.9%;	Pred. No. 1.1e-28;		
Matches	96;	Conservative 44;	Mismatches 126;	Indels 26; Gaps 5;

QY	36	LPVIYGIIFLVGGNAVVISVIFKMRPMKSTIIIMLNLA	CTDLTLTSLPFLIHYYAS	95
		: : : :	: : : :	
Db	29	LPDVSWLWVGLPNCVIAQICASRRTLTRSAVYTLNALADLL	VACSLPFLIYYAR	88
		: : : :	: : : :	
QY	96	GENWIGDPMCKEIRSFHFNLVSSILFTCFISFYCVIIHPM	SCFSIHK---TRCAVV	152
		: : : :	: : : :	
Db	89	GDHWPPGDLACRLVREFYANLHGSILFTCTISFQRYLGIC	HPAPW-HKRGGERAAWV	146
		: : : :	: : : :	
QY	153	ACAAVYIIISLVAPIMTFLLITSTNRNTRRACDLTSTSD	ELNTIKWNLIITATTFCLPLV	212
		: : : :	: : : :	

Db 147 VCGVWLVNTAQCPLTAVFAATGICQNRRTVCYDLSPILLSTRLPYLCGMALTVIGFLPFT 206
QY 213 IVTLCTVTHHTHGLQDSC-----LQKARRLTILLLLAFYVCFPLPHIL 260
Db 207 ALLACYCRMARLL-----CRQDGPAGVQAQRRSKAARMVAVVAEVIISFLPPHIT 258
QY 261 RVIRIESRL--SISCSISNQHAYIVSRPLAALNTFGNLLLVVVSDFNQ 311
Db 259 KTAIVLRSTPGVSCPVLTFFAAYKGTFRFASNSVLDILFFYFQQKFR 310

RESULT 8
151667
Thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: J51667
R;Gerszten, R.E.; Chen, J.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A;Reference number: 151667; MUID:94195429; PMID:8145852
A;Accession: J51667
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-420 <GER>
A;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:9495197; PIDN:AAA18498.1; PID:94951

Query Match 23.7%; Score 419.5; DB 2; Length 420;
Best Local Similarity 31.1%; Pred. No. 2.9e-28;
Matches 93; Conservative 73; Mismatches 108; Indels 25; Gaps 7;

QY 35 YLPVYIGIIFLVGPGNAVISTYIFKMRPKMSTIIMLNACTDLYLTLSPPLIHYA 94
Db 103 FVPSLYTVFVIGLPLNLLIIIFKMRKPAVVMNLAIADVFSVLPKIAHL 162
QY 95 SGENWIFGDMCKFRFSFHFNLSSILFCTFSIFRYCVIIHPMCSFCSIHKTRCAVVC 154
Db 163 SGNDLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVPMHLSLWRTMGRAYMAC 222
QY 155 AVWMIISLVAVIPMTFLITSTNRTNSACLDTSSDELNTIK-----WYNLLLTATTCFL- 209
Db 223 SFIWLISASTIPLLV-----TEQTKIPRLDITTCCHVDLDLKDQFY--IYFSSFCLL 276
QY 210 ----PLVTVLCYTTIHTHGLQDSCQKARRLTILLLLAFYVCFPLPHILRVIRI 265
Db 277 FFFVPIITTCYIGIISLSSSIENCKKTRALFLAVVLCVFIICFGPTNLV---- 331
QY 266 ESRLLSISCSISNQHAYIVSRPLAALNTFGNLLLVVVSDFNQAVCVSTVRC-KVS 322
Db 332 --FLTHVQLQANEFLYFAYILSACVGSVSCDPLIYVYASSQQCYLYLSLCCRKVS 387

RESULT 9
JC4800
P2Y6 receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4800; G02514
R;Communi, D.; Parentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept
A;Reference number: JC4800; MUID:96222498; PMID:8670200
A;Accession: JC4800
A;Molecule type: mRNA
A;Residues: 1-328 <COM>
A;Cross-references: UNIPROT:Q15077; EMBL:X97058
A;Experimental source: placenta
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01373
A;Accession: G02514
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 'M',4-328 <HAM>
A;Cross-references: EMBL:U52464; NID:91407632; PIDN:AAB03572.1; PID:91407633
C;Genetics:
A;Gene: P2Y6
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; placenta; receptor; transmembrane protein
F;26-52/Domain: transmembrane #status predicted <TMM1>
F;63-86/Domain: transmembrane #status predicted <TMM2>
F;104-122/Domain: transmembrane #status predicted <TMM3>
F;143-167/Domain: transmembrane #status predicted <TMM4>
F;193-216/Domain: transmembrane #status predicted <TMM5>
F;241-264/Domain: transmembrane #status predicted <TMM6>
F;283-305/Domain: transmembrane #status predicted <TMM7>
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 405; DB 2; Length 328;
Best Local Similarity 32.6%; Pred. No. 3.8e-27;
Matches 94; Conservative 44; Mismatches 140; Indels 10; Gaps 4;

QY 32 KMHLPVYIGIIFLVGPGNAVISTYIFKMRPKMSTIIMLNACTDLYLTLSPPLIHL 91
Db 25 KQLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAVYTNLALADLLYACSLPLIIY 84
QY 92 YYASGENWIFGDMCKFRFSFHFNLSSILFCTFSIFRYCVIIHPMCSFCSIHK---TR 148
Db 85 NYAQGDHWPFGFACRLVRFVYANLHGSILFCTISFQRYLGLCHPLAPW--HKRGRR 142
QY 149 CAVVACAVVMIISLVAVIPMTFLITSTNRTNSACLDTSSDELNTIKWNLILTATTC 208
Db 143 AMLVLCVAVWLAVTTQCLPTAFAATGICQNRRTVCYDLSPALATHYMPYGMALTVIGFL 202
QY 209 LPLVITVLCYTTIHTHGLQDSCQK---KARRLTILLLLAFYVCFPLPHILRVIR 264
Db 203 LPFAALLCYCLLACRLCRQDGPAPVQAQRRKARMAVVAFAAISFLPFIHTKTAY 262
QY 265 IESRL--SISCSISNQHAYIVSRPLAALNTFGNLLLVVVSDFNQ 311
Db 263 LAVRSTFGVPTVLEAFAAAYKGTFRFPASNSVLDPLIFTQTKFR 310

RESULT 10
S17148
alpha-thrombin receptor - Chinese hamster
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S17148
R;Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani
FEBS Lett. 288, 123-128, 1991
A;Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca(2
A;Reference number: S17148; MUID:91348247; PMID:1652467
A;Accession: S17148
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <RAS>
A;Cross-references: UNIPROT:Q00991; EMBL:X61958; NID:940495; PIDN:CAA43957.1; PID:94953
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 397; DB 2; Length 427;
Best Local Similarity 28.4%; Pred. No. 2.4e-26;
Matches 95; Conservative 75; Mismatches 141; Indels 24; Gaps 6;

QY 10 NASDPDYAAAFNGCTDNIPLKMH-----YLPVYIGIIFLVGPGNAV 53
Db 65 NESTLPEGRAIYLNKSHSPAPLAPFISEDAGSYTSPWLRFIPSVYTFVFWVSLPLNL 124
QY 54 VISTVIFKMRPKMSTIIMLNACTDLYLTLSPPLIHYASGENWIFGDMCKFRFSF 113
Db 125 AIAVFLVKKMKVKKPAVVTMLHLMADVLVSVLPKISYFSGSDMQFGSGMCRFATAAF 184
QY 114 HFNLYSSILFCTFSIFRYCVIIHPMCSFCSIHKTRCAVVCVAVVMIISLVAVIPMTFLIT 173
Db 195 YCNMYASIMLTVISIDRFVAVVPIQSLSWRTLGRANFTCLVIMVMAIMGVVPL--LLKR 243

QY 174 STNRT---NRSACLDLTSSDELNTI-KWYNLILTATTFCPLPVLIVVLCYTTIHTLTHGL 229
Db 244 QTRVPEGLNITTCVDVNLNLTQGFYSYFSAFVFLVPLIISICYMSIIRCLSSSS 303
QY 230 QTDSCCLKQKARLTILLALLAFVVCFLPFLHVRIRIESRLLSISCSIEHQIHEAVIVSRP 289
Db 304 VANRKSGRALFLSAVFCVFCVFCGFTNVLIMHY--LLSDSPATE-KAYFAVILLCVC 360
QY 290 LAALNTFGLNLLLYVVDNFQOAVGVSTVRCKVSGN 324
Db 361 VTSVSCIDPLIYYASSECQTLGILCKESSD 395
RESULT 11
A43448
thrombin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43448
R:Zhong, C.; Hayzer, D.J.; Corson, M.A.; Runge, M.S.
J. Biol. Chem. 267, 16975-16979, 1992
A:Title: Molecular cloning of the rat vascular smooth muscle thrombin receptor. Evidence
A:Reference number: A43448; MUID:92381002; PMID:1324917
A:Accession: A43448
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432 <ZHO>
A:Cross-references: UNIPROT:P26824; GB:M81642; NID:G207465; PIDN:AAA2274.1; PID:G207466
A:Experimental source: RASM aortic smooth muscle cells
A>Note: sequence extracted from NCBI backbone (NCBI:111973, NCBI:111974)
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 22.4%; Score 396.5; DB 2; Length 432;
Best Local Similarity 29.6%; Pred. No. 2.7e-26;
Matches 99; Conservative 74; Mismatches 141; Indels 21; Gaps 8;
QY 4 PLD-----VLNADPPDVA-----AFNGCTDENIPKMHYLPVIGIIFLVGPGNA 52
Db 73 FLEGRAVYL-NKSRPPPPPPFISDASGYLTSPWLTL---FIPSVYTFVIVSLPLNI 128
QY 53 VVIYIYFKMRPKWKSSTIIMNLACTDLYLTLSPFLIHYASGENWIFGDMCKFIKPS 112
Db 129 LAIAVFERMKVPAVVMHLMADVLVSLPFIKSYSPSGTDWQFGSGMCRFATAA 188
QY 113 FHFNYSSILFTCFISFRCYVCIHPMCSFISHKTRCAVACAVVMIISLVAVIPMTF-- 170
Db 189 CVCNMYASIMLTVISIDFLAVVPIQSLSWRTIGRANFTCVIWMVAVGVPELLKE 248
QY 171 LITSTNTRNSACDLTSSDELNTI-KWYNLILTATTFCPLPVLIVVLCYTTIHTLTHGL 229
Db 249 QTTQVPEGLNITTCVDVNLNLTQGFYSYFSAFVFLVPLIISICYMSIIRCLSSSA 308
QY 230 QTDSCCLKQKARLTILLALLAFVVCFLPFLHVRIRIESRLLSISCSIEHQIHEAVIVSRP 289
Db 309 VANRKSGRALFLSAVFCVFCVFCGFTNVLIMHY--LLSDSPGTE-TAYFAVILLCVC 365
QY 290 LAALNTFGLNLLLYVVDNFQOAVGVSTVRCKVSGN 324
Db 366 VTSVSCIDPLIYYASSECQTLGILCKESSD 400
RESULT 12
148705
proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48705
R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
A:Reference number: I48705; MUID:95197620; PMID:7890726
A:Accession: I48705
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:G663020; PIDN:CAA88097.1; PID:G66302
C:Superfamily: ATP receptor P2u
Query Match 21.9%; Score 388.5; DB 2; Length 399;
Best Local Similarity 29.9%; Pred. No. 1.2e-25;
Matches 97; Conservative 65; Mismatches 129; Indels 33; Gaps 9;
QY 35 YLPVIYGIIFLVGPGNAVIVSTYIFKMRPKWKSSTIIMNLACTDLYLTLSPFLIHYA 94
Db 79 FLVPVYIIVFVIGLPSNGMALWIFLRTKKHPPAVIYMANLALADLLSWPEFLKISYHL 138
QY 95 SGENWIFGDMCKFIKPSFHFNYSSILFTCFISFRCYVCIHPMCSFISHKTRCAVAC 154
Db 139 HGNWVYGEALCKVLIGFFYGNMYSILFMTCLSVQRYVWVIVNPMG---HPRKKANIAV 194
QY 155 AV---VWIIISLVAVIPM---TFLITSTNTRNSACDLTSSDEL-NTIKWNLILTAT 205
Db 195 GVSALAILLFLVTPILYVMKQTIYIPALNIT---TCHDVLPEEVLVGDMFNYSLSAIG 251
QY 206 TFCPLPVLIVVLCYTTIHTLTHGLQTDSCCLK--QKARLTILLALLAFVVCFLPFLHVR 263
Db 252 VFLFPALLTAGAYVLMIKTLRSSAMDEHSEKKRQRAIRLIITVLAMYFICFAPSNNLLV 311
QY 264 RIESRLLSISCSIEHQIHEAVIVSRPILAAINTFGNLLLYVVDNFPQ-----AVCSTVR 318
Db 312 ---HYFLIKTORQSHVVALYLVLCSTLNSCIDPFVYVFSKDFRDHARNALLCSYR 367
QY 319 -----CKVSGNLEQAKKISYSNN 336
Db 368 TVNRMQISLSSNKPFRKSGSYSS 391
RESULT 13
A37912
thrombin receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A37912
R:Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A:Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
A:Reference number: A37912; MUID:91168254; PMID:1672265
A:Accession: A37912
A:Molecule type: mRNA
A:Residues: 1-425 <VUA>
A:Cross-references: UNIPROT:P25116; GB:M62424; NID:G339676; PIDN:AAA36743.1; PID:G339677
C:Genetics:
A:Gene: GDB:F2R
A:Cross-references: GDB:127737; OMIM:187930
A:Map position: 5q13-5q13
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-425/Product: thrombin receptor #status predicted <MAT>
Query Match 21.9%; Score 388.5; DB 2; Length 425;
Best Local Similarity 29.3%; Pred. No. 1.3e-25;
Matches 93; Conservative 70; Mismatches 133; Indels 21; Gaps 6;
QY 35 YLPVIYGIIFLVGPGNAVIVSTYIFKMRPKWKSSTIIMNLACTDLYLTLSPFLIHYA 94
Db 104 FVPSYVYGVFVSVPLNIMALVWFLKMKVKKPAVVMHLMATADVLVSVLPFKISYF 163
QY 95 SGENWIFGDMCKFIKPSFHFNYSSILFTCFISFRCYVCIHPMCSFISHKTRCAVAC 154
Db 164 SGSDWQFGSELCRVTAFAFYCNMYASILLMTVISIDFLAVVPMQSLSWTLGRASFTC 223
QY 155 AVWIIISLVAVIPM---TFLITSTNTRNSACDLTSSDEL-NTIKWNLILTATTC 208
Db 224 LAIWALAIAGVPLVVKELQITQVPLNIT---TCHDVLNETLLEGYVAYVPSAFSAVFFF 280
QY 209 LPLVIVLCYTTIHTLTHGLQTDSCCLKQKARLTILLALLAFVVCFLPFLHVRIRIESR 268

Db 281 VPLIISTVCVSIIRCLSSAVANRSKSRALFLSAVFCIFICGPTNVLIAHYS-- 338
QY 269 LLSISCSIEHQHEAYIVSRPLAALNTFGNLLYVVVSDNFQOAVGCTVRCK----- 320
Db 339 FLGTSSTTE-AAFAYLLVCVSSISSCIDPLIYVVASSECORVYVYSILCKESSDPSSY 397
QY 321 -VSGNLEQAKKISYSNN 336
Db 398 NSSGQLMASKMDTCSSN 414
RESULT 14
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50241; J04618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.B.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: J04618; MUID:96190677; PMID:8619790
A;Accession: J04618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM2>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>
Query Match 21.5%; Score 380; DB 2; Length 308;
Best Local Similarity 30.8%; Pred. No. 4.9e-25;
Matches 90; Conservative 58; Mismatches 134; Indels 10; Gaps 6;
QY 23 NCTDENIPKMHYLVYGIIFLVGPGNAVVIYIFKMRPWKSSTIIMLNACTDILLY 82
Db 5 NCSTED-SFKYTLGCVFMSVFLGLIANCAVYIFTFLKVRNETTTMLNLAISDLIF 63
QY 83 LTSPLPLHYVAGSNWIFGDMCKCFIRFSPHFNLVSSILFLTCFSIRYCVLIHPMSCF 142
Db 64 VFTLPRYIFVY-RNWPFGDVLKISVTLFTYNNMGYSILFLTCISVDRFLAIVHFRSK 122
QY 143 SHKTRCAVACAVVWIIISLVAIVPMTFLITSTNRSACLDTSSDELNTIKWY---- 198
Db 123 TLRTRNARIVCAVWITVLASTPASP-FQSTNQNTQEQTCFENPESTWKYLSRI 181
QY 199 NILITATTCPLPLVIVTLCTYTIHILTH--GLQDSCCLKQKARLITILLAFVVCPLP 256
Db 182 VIFIEIVGFFIPLINVTCTWVRLTNKPLTLRSNKLKSKKVLKMFVHLVIFGCFVFP 241
QY 257 FHLRVRIRIESRLS--ISCSIEHQHEAYIVSRPLAALNTFGNLLYVVVSD 307
Db 242 YNITLISLMRTQTWINCWSVTVAVRTNVPVTLCAIVSNCCFPDPIVYVYFTSD 293

RESULT 15
B45680
G protein-coupled peptide receptor EBI 2 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173; PMID:8383238
A;Accession: B45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-361 <BJR>
A;Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIIP:127097)
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
Query Match 21.3%; Score 376.5; DB 2; Length 361;
Best Local Similarity 26.9%; Pred. No. 1.1e-24;
Matches 92; Conservative 70; Mismatches 159; Indels 21; Gaps 7;
QY 11 ASDP-PDYAAAFNGCTDENIPLKMHY-----LPVIYGIIFLVGPGNAVVIYIFKMR 63
Db 6 ANNETPSATPQGNDCD---LYAHHTARIVMELHYSLVFIIGLVGNLLALVVIVQNRK 61
QY 64 PWKSSTIIMLNACTDILLYTSLPFLHYVAGSNWIFGDMCKCFIRFSPHFNLVSSILF 123
Db 62 KINSTLYSTNLVISDILFTALPTRIAYVAMGDMRIGDALCRITALVFIYINTYAGVNF 121
QY 124 LTCFSIRYCVLIHPMSCFSIHKTRCAVACAVVWIIISLVAIVPMTFLITSTNRSAC 183
Db 122 MTLCSIDRFIAVHPLRYNKKRIEHAQGVCFVWILVFAQTLLPLINPMKQAEARITC 181
QY 184 LDLTSSDELNTIKWYNILITATTCPLPLVIVTLCTYTIHILTH-----THGLQDSCCLKQK 238
Db 182 MEYFNFEETKSLPILLGACFIVGVLPILIIICVYQICCKLFRKAKQNLTEKSGVNRK 241
QY 239 ARRLTILLLLAFYVCFPLPFLHVRIRIESRLLSISCSIE-NQIHEAYIVSRPLAALNTFG 297
Db 242 ALNTIILIIIVVFLCFTPYHV-AIIQHMVKKLRFSNLFECQSRHSFQISLHFTVTCIMNPN 300
QY 298 ---NLLLVVVVSDNFQOAVGCTVRCKVSGNLEQAKKISYSNN 336
Db 301 CMDPFIYFFACKGVKRWMLKQVSVSISAVKSAPEEN 342
Search completed: October 29, 2004, 15:05:21
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 14:16:02 ; Search time 192 Seconds
(without alignments)
1009.902 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSNLEQAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1771	100.0	337	1 GP80_HUMAN	Q96p68 homo sapien
2	1495	84.4	337	2 Q61YF8	Q61yf8 mus musculus
3	1495	84.4	337	2 Aat10591	Aat10591 mus muscu
4	1487	84.0	337	2 Q6Y1R5	Q6Y1r5 rattus norv
5	1487	84.0	337	2 AAP32736	Aap32736 rattus no
6	579	32.7	373	2 Q8BMJ5	Q8bmj5 mus musculus
7	577.5	32.6	357	2 Q9DE05	Q9de05 raja erinac
8	576	32.5	373	1 P2YR_CAVPO	P59902 cavia porce
9	575	32.5	373	1 P2YR_MOUSE	P49650 mus musculus
10	575	32.5	373	2 BAC28413	Bac28413 mus muscu
11	575	32.5	373	2 BAC29506	Bac29506 mus muscu
12	567	32.0	373	1 P2YR_HUMAN	P47900 homo sapien
13	565.5	31.9	362	1 P2YR_CHICK	P34996 gallus gall
14	565.5	31.9	362	1 P2YR_MELGA	P49652 meleagris g
15	565	31.9	373	1 P2YR_RAT	P49651 rattus norv
16	562	31.7	373	1 P2YR_BOVIN	P48042 bos taurus
17	559	31.6	537	2 Q7ZW07	Q7zwq7 xenopus lae
18	557	31.5	537	1 P2Y8_YENLA	P79928 xenopus lae
19	556.5	31.4	361	2 Q90X57	Q90x57 xenopus lae
20	547	30.9	374	2 O57466	O57466 meleagris g
21	537	30.3	347	2 Q7Z2A4	Q7zza4 brachydanio
22	532.5	30.1	349	2 Q6P852	Q6p852 xenopus tro
23	532.5	30.1	349	2 AAH61378	AAh61378 xenopus t
24	514	29.0	365	1 P2Y4_HUMAN	P51582 homo sapien
25	512	28.9	361	1 P2Y4_RAT	O35811 rattus norv
26	503	28.4	361	1 P2Y4_MOUSE	O35811 rattus norv
27	503	28.4	361	2 BAC36314	Bac36314 mus muscu
28	492	27.8	328	1 P2Y3_CHICK	Q89907 gallus gall
29	488.5	27.6	317	2 Q61YF9	Q61yf9 rattus norv
30	488.5	27.6	317	2 Aat10590	Aat10590 rattus no
31	487.5	27.5	346	1 CLT2_HUMAN	Q9ns75 homo sapien

RESULT 1

GP80_HUMAN

ID GP80_HUMAN STANDARD; PRT; 337 AA.

AC Q96P68; Q86TL1;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide

DE receptor) (P2Y-like GPCR).

GN Name=GPR80; Synonyms=GPR99;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,

RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor

RT genes.";

RL Gene 275:83-91(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX PubMed=12098360;

RA Wittenberger T., Hellebrand S., Munc A., Kreienkamp H.-J.,

RA Schaller H.C., Hampe W.;

RT "GPR99, a new G protein-coupled receptor belonging to a new subgroup

RT of nucleotide receptors.";

RN BMC Genomics 3:17-17(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22040266; PubMed=12044878;

RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

RT "Identification of G protein-coupled receptor genes from the human

RT genome sequence.";

RL FEBS Lett. 520:97-101(2002).

RN [4]

RP SEQUENCE FROM N.A.

RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,

RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;

RT "Genome-wide discovery and analysis of human seven transmembrane helix

RT receptor genes.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Thyroid;

RA Brues M., Bonisch H., von Kugelgen I.;

RT "Molecular cloning and functional characterization of a new human P2Y

RT receptor.";

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Orphan receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

Aah69160 homo sapi
O93361 meleagris g
P41232 rattus norv
Aah61754 rattus no
Q9bxa5 homo sapien
P35383 mus musculu
P41231 homo sapien
Q95n03 sus scrofa
Q8r528 mus musculu
Q920a1 mus musculu
Q924t9 rattus norv
Q63371 rattus norv
Aah72520 rattus no
Q9erk9 mus musculu

ALIGNMENTS

CC -!- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, in
 CC placenta. Not detected in brain tissues including the frontal
 CC cortex, caudate putamen, thalamus, hypothalamus, hippocampus or
 CC pons.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF411109; AAL26480.1; -;
 DR EMBL; AF370886; AAM76912.1; -;
 DR EMBL; AB083598; BAB89311.1; -;
 DR EMBL; AB065877; BAC06095.1; -;
 DR EMBL; AJ305372; CAC83857.1; -;
 DR Genew; HGNC:4531; GPR80.
 DR MIM; 606922; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR002286; P2_purinocptn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 34
 FT TRANSMEM 35 55
 FT DOMAIN 56 69
 FT TRANSMEM 70 90
 FT DOMAIN 91 116
 FT TRANSMEM 117 137
 FT DOMAIN 138 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 201
 FT TRANSMEM 202 222
 FT DOMAIN 223 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 284
 FT TRANSMEM 285 305
 FT DOMAIN 306 337
 FT DISULFID 106 183
 FT CARBOHYD 10 10
 FT CARBOHYD 23 23
 FT CARBOHYD 176 176
 FT CARBOHYD 179 179
 FT CONFLICT 14 14
 FT CONFLICT 236 236
 FT CONFLICT K -> R (in Ref. 5).
 SQ SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

Query Match 100.0%; Score 1771; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 3.3e-112;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDFMCKFRFSFHNLYSS 120
 DB 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDFMCKFRFSFHNLYSS 120
 QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNTRN 180
 DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNTRN 180
 QY 181 SACDLTSSDELTNTIKWYNLILTATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240
 DB 181 SACDLTSSDELTNTIKWYNLILTATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240
 QY 241 RLTIILLAFYVCFLPFHILRVIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFYVCFLPFHILRVIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300

RESULT 3
 AAT10591
 ID AAT10591 PRELIMINARY; PRT; 337 AA.
 AC AAT10591;

DB 241 RLTIILLAFYVCFLPFHILRVIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVSDFNQAVCSVTRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVSDFNQAVCSVTRCKVSGNLEQAKKISYNNP 337

RESULT 2

QY Q61YF8 PRELIMINARY; PRT; 337 AA.
 AC Q61YF8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE G-protein-coupled receptor 99.
 GN Name=Gpr39;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA He W., Miao F.J.P., Lin D.C.H., Schwandner R.T., Wang Z., Gao J.,
 RA Chen J.-L., Tian H., Ling L.;
 RA "Citric Acid Cycle Intermediates as Ligands for Orphan G-Protein-
 RT Coupled Receptors.";
 RL Nature 0.0-0(2004).
 DR EMBL; AY612852; AAT10591.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR002286; P2_purinocptn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR01157; P2_PURINOCPTN.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 337 AA; 38230 MW; 079A603551112277 CRC64;

Query Match 84.4%; Score 1495; DB 2; Length 337;
 Best Local Similarity 85.5%; Pred. No. 1.6e-93;
 Matches 288; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPLDYLANASDFPDYAAFGNCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDFMCKFRFSFHNLYSS 120
 DB 61 KMRPKSSTIIMNLACTDLYLTSPLFIHYASGENWIFGDFMCKFRFSFHNLYSS 120
 QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNTRN 180
 DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTSTNTRN 180
 QY 181 SACDLTSSDELTNTIKWYNLILTATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240
 DB 181 SACDLTSSDELTNTIKWYNLILTATTCPLPLVITLCYTTIIHTLTHGLQDSCCLKQKAR 240
 QY 241 RLTIILLAFYVCFLPFHILRVIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFYVCFLPFHILRVIRIESRLISCSIEHQHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVSDFNQAVCSVTRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVSDFNQAVCSVTRCKVSGNLEQAKKISYNNP 337

RESULT 3
 AAT10591
 ID AAT10591 PRELIMINARY; PRT; 337 AA.
 AC AAT10591;


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Db 61 KMRPWKSTTLMNLAALDLYLTLSPFLIHYVAGENWIFGDFMCKFIKRFHFNLYSS 120
QY 121 ILFLTCFSIRYCVIIHPMCSFSTHKTCAVAVVWISLVAIVMTFLTITSTNTR 180
Db 121 ILFLTCFSIRYCVIIHPMCSFSTHKTCAVAVVWISLVAIVMTFLTITSTNTR 180
QY 181 SACLDTSSDELNTIKWNMLTATTTCLPIVIVTLCYTTIHTLTHGLQDSCCLKOKAR 240
Db 181 SACLDTSSDELNTIKWNMLTATTTCLPIVIVTLCYTTIHTLTHGLQDSCCLKOKAR 240
QY 241 RLTLILLAFVVCFLPHILIRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTLILLAFVVCFLPHILIRVIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVVSNFQAVCVTRCKVSGNLEQAKKISYNP 337
Db 301 LYVVVSNFQAVCVTRCKVSGNLEQAKKISYNP 337
RESULT 6
Q8BMJ5 PRELIMINARY; PRT; 373 AA.
ID Q8BMJ5
AC Q8BMJ5;
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:5730548K21 product:P2Y PURINOCEPTOR 1, full insert
DE sequence.
GN Name=P2ry1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC STRAIN=C57BL/6J; TISSUE=Whole body;
ADACHI J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehli Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Toyata T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AK030759; BAC27125.1; -
MGI; MGI-105049; P2ry1.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045028; F: purinergic nucleotide receptor activity; G-...; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000142; P2Y_Rhodopsn.
DR InterPro; IPR002286; P2Y_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR00595; P2Y_Rhodopsn.
DR PRINTS; PR01157; P2Y_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_2; 1.
SEQUENCE 373 AA; 42228 MW; BA88124B/847287C CRC64;
Query Match 32.7%; Score 579; DB 2; Length 373;
Best Local Similarity 36.8%; Pred. No. 1.7e-31;
Matches 110; Conservative 66; Mismatches 119; Indels 4; Gaps 2;
QY 24 CTDENIPKMYLPIVYIGIILVGFPGNAVISTVIFKMRPKSSTIIMNLACTDLYL 83
Db 42 CALTKTGFQYVLPVAVIIVFIIGLSVAVIMVVFHMKPWSGVSVNFMALADFLV 101
QY 84 TSLPFLIHYVAGENWIFGDFMCKFIKRFHFNLYSSILFTCFIFRYCVIIHPMCSFS 143
Db 102 LTPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSLFTLCISAHRYSGVVYPLKSLG 161
QY 144 IHKTRCAVVACVWVWISLVAIVMTFLTITSTNTRNS-ACLDLTSSDELNTIKWNLL 202
Db 162 RLKKKNVAVSVLWLVVWVVAISPIFYSGTGRKNKVTCTYDTTSDNLYRSFYISMCT 221
QY 203 TATTECLPIVIVTLCYTTIHTLTHGLQDSCCLKOKARLTLILLAFVVCFLPHILRV 262
Db 222 TVAMFCIPLVLILGCVGLIVKALVNDLNSPLRKRGIYLVIVITVFAVSTPIPHVMKT 281
QY 263 IRIESRL--LSISCSIEHQHEAVIVSRPLAALNTFGNLLYVVVSNFQAVCVSTR 318
Db 282 MNLRLDLFQPTMCDNFDRVATVQVTFGLASLNSCVDPIYFLAGDTFRRLSRATR 340
RESULT 7
Q9DE05 PRELIMINARY; PRT; 357 AA.
ID Q9DE05
AC Q9DE05;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE P2Y receptor.
OS Raja erinacea (Little skate).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
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[illegible]

Db 102 LTPALIFYYFNKTDWIFGDMCKLQRFIFHVNLYGSLFTICSAHRYSGVVYPLKSLG 161
 QY 144 IHKTRCAVACAVVWLIISAVIPMTFLTSTNTRNS-ACLDLTSSDELNTIKWNIL 202
 Db 162 RLKKNAICISVWLVVISPILFYSGTGRNKTITCDDTSDEYRSFYISMT 221
 QY 203 TATTFCLPLVIVTCLYTTIHTLTHGLQDSCIKOKARLTILLIAFYVCPFLPHILRV 262
 Db 222 TVAMFCVPLVILGCVGLIVRALIVKLDNSPLRRKSIYLVILVTFAVSIPIHVMKT 281
 QY 263 IRIEISRL---LSISCSIQENIHEIVSRPLAALTFGNLLYVVVDSNFOQAVCSVTR 318
 Db 282 MNLRLARLDQTPAMCAFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRLSRATR 340

RESULT 13

P2YR_CHICK
 ID P2YR_CHICK STANDARD; PRT; 362 AA.
 AC P34996;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
 GN Name=P2Y1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93285340; PubMed=8508924;
 RA Webb T.E., Simon J., Krishak B.J., Bateson A.N., Smart T.G.,
 RT King B.F., Burnstock G., Barnard E.A.;
 RT "Cloning and functional expression of a brain G-protein-coupled ATP
 receptor.";
 RL FEBS Lett. 324:219-225 (1993).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=97026278; PubMed=8872457;
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
 RT "Modelling the P2Y purinoceptor using rhodopsin as template.";
 RL Drug Des. Discov. 13:133-140 (1995).
 CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
 ATP and ADP. Seems to mediate its action via a pertussis toxin
 insensitive G-protein, probably belonging to the Gq family that
 activate a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain, spinal cord, gastrointestinal tract,
 spleen and leg muscle. Is not detected in the heart, liver,
 stomach, lung and kidney.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X73268; CAA51716.1; -.
 DR PIR; S33733; S33733.
 DR PDB; 1DDD; Model; 1-39-71, 2-75-104, 3-113-139, 4-152-180, 5-203-233, 6-248-277, 7-
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000142; P2Y_purinocptor.
 DR InterPro; IPR002286; P2_purinocptor.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RCEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RCEP_F1_2; 1.
 KW 3D-structure; G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 41 Extracellular (Potential).
 FT TRANSMEM 42 63 1 (Potential).
 FT DOMAIN 64 76 Cytoplasmic (Potential).
 FT TRANSMEM 77 98 2 (Potential).
 FT DOMAIN 99 115 Extracellular (Potential).
 FT TRANSMEM 116 136 3 (Potential).
 FT DOMAIN 137 155 Extracellular (Potential).
 FT TRANSMEM 156 177 4 (Potential).
 FT DOMAIN 178 207 Extracellular (Potential).
 FT TRANSMEM 208 227 5 (Potential).
 FT DOMAIN 228 254 Cytoplasmic (Potential).
 FT TRANSMEM 255 274 6 (Potential).
 FT DOMAIN 275 292 Extracellular (Potential).
 FT TRANSMEM 293 317 7 (Potential).
 FT DOMAIN 318 362 Cytoplasmic (Potential).
 FT DISULFID 113 191 By similarity.
 FT CARBOHYD 11 11 N-linked (GlcNAc..) (Potential).
 FT CARBOHYD 26 26 N-linked (GlcNAc..) (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc..) (Potential).
 FT CARBOHYD 186 186 N-linked (GlcNAc..) (Potential).
 FT HELIX 42 69
 FT HELIX 77 102
 FT HELIX 115 137
 FT HELIX 154 178
 FT HELIX 205 231
 FT HELIX 250 275
 FT HELIX 290 305
 FT TURN 306 307
 FT HELIX 308 320
 SQ SEQUENCE 362 AA; 41194 MW; A806C88FB9514761 CRC64;
 Query Match 31.9%; Score 565.5; DB 1; Length 362;
 Best Local Similarity 35.0%; Pred. No. 1.4e-30;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;
 QY 1 MNEPDIYLANASDFDYAA---AFGN---CTDENIPLKMHVLPVYIGIIFLNGFPGNAV 53
 Db 1 MTEALISAALNGTQPELLAGWAGNATKSLTKGTFQFYLPVYILVITGFLGNSV 60
 QY 54 VISTYIFQMRPWKSTIIMLNACTDLYLTLPLIHYASGENWIFGDFMCKFIRFSF 113
 Db 61 AIWPFVHMRFWSGISVYMFNLALADFLYVLTLPALIFYENKTDWIFGDMCKLQRF 120
 QY 114 HFNLYSSILFTCSIFHYCVIIHPMSCFSIHKTRCAVACAVWIIISLVAIPMTFLI- 172
 Db 121 HVNLYGSLFTCSVHRITGVHPLKSLGRKKNVYVSVSLVWALVAVIAPILFYSG 180
 QY 173 TSTNTRNSACLDLTSSDELNTIKWNILITATTPCLPLVITVLCYTTIHTLHGLQTD 232
 Db 181 TGVRNKTITCYDTADEYLASYFYVSMCTTFWECIPFVILGCGYGLIVKALIKDLN 240
 QY 233 SCLQKARLTILLIAPYVCFPLPHILRVIRISRL---LSISCSIQENIHEAVISRP 289
 Db 241 SPLRRKSIYLVILTVFAVSYPFHVMKTLNRLRLDQTPQMFNDKVVATYQVTRG 300
 QY 290 LAALNTFCNLLYVVVDSNFOQAVCSVTR 318
 Db 301 LASLNSCVDPIYFLAGDTFRRLSRATR 329

RESULT 14

P2YR_MELGA
 ID P2YR_MELGA STANDARD; PRT; 362 AA.
 AC P49652;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1
 DE orphan receptor).
 GN Name=P2Y1;
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.

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OX NCBI_TaxID=9103;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94335907; PubMed=8058061;
RA Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
RT "Expression of a cloned P2Y purinergic receptor that couples to
RT phospholipase C.";
RL Mol. Pharmacol. 46:8-14 (1994).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97382456; PubMed=9240460;
RA Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
RT "The 6H1 orphan receptor, claimed to be the P2Y5 receptor, does not
RT mediate nucleotide-promoted second messenger responses.";
RL Biochem. Biophys. Res. Commun. 236:455-460 (1997).
CC -1- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. Seems to mediate its action via a pertussis toxin
CC insensitive G-protein, probably belonging to the Gq family that
CC activate a phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Mainly found in blood, brain, and lung. To a
CC lesser extent in stomach, gut and skeletal muscle.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
EMBL; U09842; AAA18784.1; -.
DR HSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000142; P2Y_purinocptor.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 41 Extracellular (Potential).
FT TRANSMEM 42 61 1 (Potential).
FT DOMAIN 64 76 Cytoplasmic (Potential).
FT TRANSMEM 77 98 2 (Potential).
FT DOMAIN 99 115 Extracellular (Potential).
FT TRANSMEM 116 136 3 (Potential).
FT DOMAIN 137 155 Cytoplasmic (Potential).
FT TRANSMEM 156 177 4 (Potential).
FT DOMAIN 178 207 Extracellular (Potential).
FT TRANSMEM 208 228 5 (Potential).
FT DOMAIN 228 254 Cytoplasmic (Potential).
FT TRANSMEM 255 274 6 (Potential).
FT DOMAIN 275 292 Extracellular (Potential).
FT TRANSMEM 293 317 7 (Potential).
FT DOMAIN 318 362 Cytoplasmic (Potential).
FT DISULFID 113 191 By similarity.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9B64349C CRC64;

Query Match 31.9%; Score 565.5; DB 1; Length 362;
Best Local Similarity 35.0%; Pred. No. 1.4e-30;
Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 1 MNEPLDYLANASDFPDYAA---AFGN---CTDENILPKMHVLPVYIGLIVLWGFPGNAV 53
DB 1 MTEALISALNGTQPELLAGGWAAGNASTKSLTKTGQFYPLVTVYILVITGFLGNSV 60

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QY 54 VISTYIFKMRPKSSTIIMLNACTDLYLTSLPFLIHYYASGNWIFGDMCKFIKFSF 113
DB 61 AIWMFVHMPWNSGISVYMFENLADFLVLTLPALIFYFYNTKDMIFGDMCKLQRFIF 120
QY 114 HFNLYSILFLTCFSIFRYCVIIHPMSCFSIHTRCAVACAVVWISLVAVIPMTFLI - 172
DB 121 HVNLYGSILFLTCISVHRVTGVVHPLKSLGRKKQNAVYVSSLVWALVAVIAPILFYS 180
QY 173 TSTNRTNSACLDITSSDELNTIKWYNLILATATTECLPLVITLCYTTIITHTHGLQTD 232
DB 181 TGVRRNKITCYDTTADDEYLRVYFVSMCTVMFCIPFIVILGCYGLIYKLDLN 240
QY 233 SCLQKARRITILLALAFYVCFPLPHILIRVIRIESRL---LSISCSNIENIHEAYIVSRP 289
DB 241 SPLRRKSYLVIIIVLTVFAVSYPFPHVMKTLNLRALDFTQPMCAFNKDVYATYQVTRG 300
QY 290 LAALTFGNLLLYVVDNFQQAQVCSVTR 318
DB 301 LASINSCVDPILYPLAGDTFRRLSRATR 329

RESULT 15
ID P2YR RAT STANDARD; PRT; 373 AA.
AC P49651;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE P2Y purinocptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN Name=P2Y1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Insulinoma;
RX MEDLINE=95298025; PubMed=7779087;
RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT "Cloning of rat and mouse P2Y purinocptors."
RL Biochem. Biophys. Res. Commun. 211:211-218 (1995).
CC -1- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. In pancreatic islets, may mediate some of the effects
CC of extracellular ATP on insulin secretion.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in muscle, heart, liver, kidney,
CC lung, brain, spleen, but not in testis.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
EMBL; U22830; AAA91303.1; -.
DR HSP; P34996; 1DDD.
DR RGD; 3242; P2Y1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000142; P2Y_purinocptor.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 52 Extracellular (Potential).
FT TRANSMEM 53 74 1 (Potential).
FT DOMAIN 75 87 Cytoplasmic (Potential).
FT TRANSMEM 88 109 2 (Potential).

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FT	DOMAIN	110	126	Extracellular (Potential).	
FT	TRANSMEM	127	147	3 (Potential).	
FT	DOMAIN	148	166	Cytoplasmic (Potential).	
FT	TRANSMEM	167	188	4 (Potential).	
FT	DOMAIN	189	218	Extracellular (Potential).	
FT	TRANSMEM	219	238	5 (Potential).	
FT	DOMAIN	239	265	Cytoplasmic (Potential).	
FT	TRANSMEM	266	285	6 (Potential).	
FT	DOMAIN	286	303	Extracellular (Potential).	
FT	TRANSMEM	304	328	7 (Potential).	
FT	DOMAIN	329	373	Cytoplasmic (Potential).	
FT	DISULFID	124	202	By similarity.	
FT	CARBOHYD	11	11	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	27	27	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	113	113	N-linked (GLCNAC. . .) (Potential).	
FT	CARBOHYD	197	197	N-linked (GLCNAC. . .) (Potential).	
FT	SEQUENCE	373 AA;	42321 MW;	6DDP676287B5E648 CRC64;	
Query Match					
Best Local Similarity					31.98; Score 565; DB 1; Length 373;
Matches 107; Conservative					36.8%; Pred. No. 1.5e-30;
					Mismatches 113; Indels 4; Gaps 2;
QY	32	KMHPYVIYGIIFLVGPGNAVISTVIFKMRPMKSTIIMLNACTDLYLTSLPFLIH	91		
Db	50	QFYLLPAVYILVFIIGLNGSVALWMEVFHKPMGSGISVMFNALADFLVLTLPALIF	109		
QY	92	YYASGENWIPGDPWCKEPIRFSFHNLYSSILFTFCFSIFRYCVIIHPMCSFCSIHKTRCAV	151		
Db	110	YYFNKTDWIPGDPWCKLQRFIFHVNLYGSLFTFCISAHRYSGVVYPLKSLGRUKKNAI	169		
QY	152	VACAVVWIIISLVAIPMTLITSTNNRNS-ACLDLTSSDELNTIKWNLLITATTCLP	210		
Db	170	YVSVLWLVIVVVAISPLFTVSGTIRKKNVTVCYDSTSDSELYRSFYIYSCMTTVA	229		
QY	211	LVITVLCYTTIITHLTGLODTSCLKQKARRLTILLLEAFVVCFLPFIHLIRVIRIESRL-	269		
Db	230	LVLILGCGLIVRALIYKOLDNSPLRKSIVLVIIVLTVAVSYPFHVMTKWNLRALD	289		
QY	270	--LSISCSSTENOIHEAYIVSRPLAALNFGNLLLYVVVSNFQAVCGSTVR	318		
Db	290	FQTPMPCDNDNRVYATYQVTRGLASLNSCVDPILFYFLAGDTFRRLRGRATF	340		

Search completed: October 29, 2004, 15:04:33
Job time : 194 secs

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OM protein - protein search, using sw model

Run on: October 29, 2004, 14:50:53 ; Search time 141 Seconds
(without alignments)
774.899 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSGNLEQAKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1771	100.0	337	9	US-09-943-798-4
2	1771	100.0	337	10	US-09-885-453-1
3	1771	100.0	337	14	US-10-023-775B-2
4	1771	100.0	337	14	US-10-270-144-2
5	1771	100.0	337	14	US-10-188-405-8
6	1771	100.0	337	14	US-10-079-384-14
7	1771	100.0	337	14	US-10-278-141-2
8	1771	100.0	337	14	US-10-017-161-526
9	1771	100.0	337	14	US-10-010-568-2
10	1771	100.0	337	14	US-10-321-807-28
11	1771	100.0	337	14	US-10-296-081-2
12	1771	100.0	337	14	US-10-375-157-2
13	1771	100.0	337	14	US-10-292-798-464

14	1771	100.0	337	14	US-10-023-634-6	Sequence 6, Appli
15	1771	100.0	337	14	US-10-023-634-57	Sequence 57, Appli
16	1771	100.0	337	15	US-10-055-569A-8	Sequence 8, Appli
17	1771	100.0	337	15	US-10-344-728-2	Sequence 2, Appli
18	1771	100.0	337	15	US-10-343-650A-14	Sequence 14, Appli
19	1771	100.0	337	16	US-10-321-807-28	Sequence 28, Appli
20	1771	100.0	337	16	US-10-763-854-2	Sequence 2, Appli
21	1771	100.0	337	16	US-10-314-048A-28	Sequence 28, Appli
22	1771	100.0	337	17	US-10-775-965-111	Sequence 11, App
23	1764	99.6	337	14	US-10-225-567A-647	Sequence 647, App
24	1764	99.6	337	14	US-10-400-991-16	Sequence 16, Appl
25	1602.5	90.5	336	10	US-09-782-974C-86	Sequence 86, Appl
26	1444	81.5	276	9	US-09-943-798-2	Sequence 2, Appli
27	881.5	49.8	179	15	US-10-276-774-1452	Sequence 1452, Ap
28	831.5	47.0	192	10	US-09-782-974C-60	Sequence 60, Appl
29	575	32.5	299	14	US-10-270-144-4	Sequence 4, Appli
30	575	32.5	373	14	US-10-010-568-5	Sequence 5, Appli
31	575	32.5	373	14	US-10-375-157-5	Sequence 5, Appli
32	575	32.5	373	14	US-10-023-634-58	Sequence 58, Appl
33	575	32.5	373	15	US-10-055-569A-50	Sequence 50, Appl
34	567	32.0	373	10	US-09-745-842-14	Sequence 14, Appl
35	567	32.0	373	14	US-10-092-135-6	Sequence 6, Appli
36	567	32.0	373	14	US-10-225-567A-219	Sequence 219, App
37	567	32.0	373	14	US-10-010-568-8	Sequence 8, Appli
38	567	32.0	373	14	US-10-375-157-8	Sequence 59, Appl
39	567	32.0	373	14	US-10-023-634-59	Sequence 51, Appl
40	567	32.0	373	15	US-10-055-569A-51	Sequence 6, Appli
41	567	32.0	373	15	US-10-344-728-6	Sequence 28, Appl
42	565.5	31.9	362	10	US-09-779-679-28	Sequence 3, Appli
43	565.5	31.9	362	10	US-09-991-225-3	Sequence 4, Appli
44	565.5	31.9	362	10	US-09-991-225-4	Sequence 3, Appli
45	565.5	31.9	362	14	US-10-092-135-3	

ALIGNMENTS

RESULT 1

US-09-943-798-4

; Sequence 4, Application US/09943798

; Patent No. US20020065215A1

; GENERAL INFORMATION:

; APPLICANT: Glaxo Group Limited

; TITLE OF INVENTION: Polypeptide

; FILE REFERENCE: QG1021

; CURRENT APPLICATION NUMBER: US/09/943,798

; CURRENT FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-943-798-4

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNEPLDYLANASDFPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF	60
Db	1	MNEPLDYLANASDFPDYAAAFGNCCTDENIPKMHYLPVIYGIIFLVGPGNAVISTYIF	60
Qy	61	KMRPKWSSTIIMLNACTDILLYLSLPPLIHYASGENWIFGDFMCKTIRSFHENLYSS	120
Db	61	KMRPKWSSTIIMLNACTDILLYLSLPPLIHYASGENWIFGDFMCKTIRSFHENLYSS	120
Qy	121	ILFLTCFSIFRYCVIIHPMSCFSTHKTCVAVVAVVWIIISIVAVIPMTFLTSTNRNR	180
Db	121	ILFLTCFSIFRYCVIIHPMSCFSTHKTCVAVVAVVWIIISIVAVIPMTFLTSTNRNR	180
Qy	181	SACDLTSSDELNTIKWYNLIITATFTCLPLVITLCVYTTIITHTLTHGLQDSCILKQKAR	240
Db	181	SACDLTSSDELNTIKWYNLIITATFTCLPLVITLCVYTTIITHTLTHGLQDSCILKQKAR	240

Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240
Qy 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337
RESULT 2
US-09-885-453-1
; Sequence 1, Application US/09885453
; Publication No. US2003008080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRxl0
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: amino acid sequence GPCRxl0
; LOCATION: (1)..(337)
; OTHER INFORMATION: GPCRxl0 amino acid sequence
US-09-885-453-1

Query Match 100.0%; Score 1771; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIF 60
Qy 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120
Db 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120
Qy 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Qy 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240
Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240
Qy 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337

RESULT 3
US-10-023-775B-2
; Sequence 2, Application US/10023775B
; Publication No. US2003002282A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (BP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EB except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US2003002282A1el Polypeptide

; FILE REFERENCE: PC10959AGPR
; CURRENT APPLICATION NUMBER: US/10/023,775B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030854.4
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,590
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/296,660
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: GB 0111031.1
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-775B-2
Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVYIGIIFLVGPGNAVVISYIF 60
Qy 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120
Db 61 KMRPKSSTIIMNLACTDLILYLSPLFIHYASGENWIFGDFMCKFIRESFHNLYSS 120
Qy 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Qy 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240
Db 181 SACLDTSSDELNTIKWYNLILATTTCLPLVIVTLCTYTIHTLTHGLQDSCCLKQKAR 240
Qy 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTLILLAFVVCFLPHILRVIRIESRLISCSIQENQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVDNFOQAVGCVTRCKVSGNLEQAKKISYNNP 337
RESULT 4
US-10-270-144-2
; Sequence 2, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-10-270-144-2
Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
QY 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240
DB 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240
QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

RESULT 5

US-10-188-405-8

; Sequence 8, Application US/10188405

; Publication No. US20030082585A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Hui

; APPLICANT: Dai, Kang

; APPLICANT: Chen, Jin-Long

; APPLICANT: Zhao, Jiagang

; APPLICANT: Cutler, Gene

; APPLICANT: Tularik Inc.

; TITLE OF INVENTION: No. US20030082585A1el Receptors

; FILE REFERENCE: 018781-00841005

; CURRENT APPLICATION NUMBER: US/10/188,405

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US 60/302,800

; PRIOR FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 8

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human TGR164

US-10-188-405-8

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
QY 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240
DB 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240

QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

RESULT 6

US-10-079-384-14

; Sequence 14, Application US/10079384

; Publication No. US20030108986A1

; GENERAL INFORMATION:

; APPLICANT: Communi, Didier

; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: 9409/2132

; CURRENT APPLICATION NUMBER: US/10/079,384

; CURRENT FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 09/885,453

; PRIOR FILING DATE: 2001-06-20

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 14

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-079-384-14

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
DB 61 KMRPKSSTIIMNLACTDLYLTSPLFLHYHAYASGENWIFGDMCKFRFSFHNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLTITSTNR 180
QY 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240
DB 181 SACDLTSSDELTIKWNLITATTCLPLVIVTLCTYIIHTLTHGLQDSCCLKQAR 240
QY 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300

QY 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

DB 301 LYVVSDNFQAVGCVTRCKVSGNLEQAKKISYNNP 337

RESULT 7

US-10-278-141-2

; Sequence 2, Application US/10278141

; Publication No. US20030138818A1

; GENERAL INFORMATION:

; APPLICANT: PATTERSON, Chandra

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: THORNTON, Michael

; APPLICANT: LU, Yan

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: GRAUL, Richard

; APPLICANT: KHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: WALIA, Narinder K.

; APPLICANT: NGUYEN, Dannel B.

; APPLICANT: YUE, Henry
; APPLICANT: HAPALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 USA
; CURRENT APPLICATION NUMBER: US/10/278,141
; CURRENT FILING DATE: 2002-10-21
; PRIOR FILING DATE: 60/208,834
; PRIOR FILING DATE: 2000-06-02
; PRIOR FILING DATE: 60/207,566
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 60/162,885
; PRIOR FILING DATE: 2001-05-17
; PRIOR FILING DATE: 60/205,628
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 60/208,861
; PRIOR FILING DATE: 2000-06-02
; PRIOR FILING DATE: 60/206,222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030138818A1 6575963CD1
US-10-278-141-2

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60
Qy 61 KMRPWKSTIIMLNACTDLYLTSLPFLHYHAYASGENWIFGDMCKFIKIRSFHFNLYSS 120
Db 61 KMRPWKSTIIMLNACTDLYLTSLPFLHYHAYASGENWIFGDMCKFIKIRSFHFNLYSS 120
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAVIPIMTFLITSTNTR 180
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAVIPIMTFLITSTNTR 180
Qy 181 SACLDLTSSDELNTIKWYNILITATTCPLPLVIVTLCTYIIHTLTHGLQDSCCLKOKAR 240
Db 181 SACLDLTSSDELNTIKWYNILITATTCPLPLVIVTLCTYIIHTLTHGLQDSCCLKOKAR 240
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337
Db 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 8
US-10-017-161-526
; Sequence 526, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 526
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-526

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60
Qy 61 KMRPWKSTIIMLNACTDLYLTSLPFLHYHAYASGENWIFGDMCKFIKIRSFHFNLYSS 120
Db 61 KMRPWKSTIIMLNACTDLYLTSLPFLHYHAYASGENWIFGDMCKFIKIRSFHFNLYSS 120
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAVIPIMTFLITSTNTR 180
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVWIIISLVAVIPIMTFLITSTNTR 180
Qy 181 SACLDLTSSDELNTIKWYNILITATTCPLPLVIVTLCTYIIHTLTHGLQDSCCLKOKAR 240
Db 181 SACLDLTSSDELNTIKWYNILITATTCPLPLVIVTLCTYIIHTLTHGLQDSCCLKOKAR 240
Qy 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAPYVCFPLPHILVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337
Db 301 LYVVDNFOQAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 9
US-10-010-568-2
; Sequence 2, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY23, EXPRESSED HIC
; FILE REFERENCE: D0077 NP
; CURRENT APPLICATION NUMBER: US/10/010,568
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/269,795
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-010-568-2

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVVIYIF 60

QY 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120
Db 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120
QY 121 ILFTCFISFRYCVIIHPMSCFSIHKTRCAVACAVVMIISLVAVIPMTFLTSTNRTNR 180
Db 121 ILFTCFISFRYCVIIHPMSCFSIHKTRCAVACAVVMIISLVAVIPMTFLTSTNRTNR 180
QY 181 SACDLTSSDELNTIKWYNLILTATTCFCLPLVIVITLCVTTIIHTLTHGLQDSCCLKQKAR 240
Db 181 SACDLTSSDELNTIKWYNLILTATTCFCLPLVIVITLCVTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTIILLAFVYCFPHILVRIRIESRLLSISCSIEHQHEAYIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAFVYCFPHILVRIRIESRLLSISCSIEHQHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 10
US-10-321-807-28
; Sequence 28, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-28

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAFNCCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNCCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120

Db 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120
QY 121 ILFTCFISFRYCVIIHPMSCFSIHKTRCAVACAVVMIISLVAVIPMTFLTSTNRTNR 180
Db 121 ILFTCFISFRYCVIIHPMSCFSIHKTRCAVACAVVMIISLVAVIPMTFLTSTNRTNR 180
QY 181 SACDLTSSDELNTIKWYNLILTATTCFCLPLVIVITLCVTTIIHTLTHGLQDSCCLKQKAR 240
Db 181 SACDLTSSDELNTIKWYNLILTATTCFCLPLVIVITLCVTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTIILLAFVYCFPHILVRIRIESRLLSISCSIEHQHEAYIVSRPLAALNTFGNLL 300
Db 241 RLTIILLAFVYCFPHILVRIRIESRLLSISCSIEHQHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 11
US-10-296-081-2
; Sequence 2, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAPALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 PCT
; CURRENT APPLICATION NUMBER: US/10/296,081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,861
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030220477A1 6575963CD1
US-10-296-081-2

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAFNCCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNCCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120
Db 61 KMRPKSSTIIMLNACTDLYLTSLPFLIHYASGENWIFGDMCKFIRFSFHNLYSS 120

QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
QY 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
DB 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337
DB 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337

RESULT 12

US-10-375-157-2
; Sequence 2, Application US/10375157
; Publication No. US20030224458A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY23, EXPRESSED
; FILE REFERENCE: D0077A CIP
; CURRENT APPLICATION NUMBER: US/10/375,157
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 10/010,568
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/269,795
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-375-157-2

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHVLPVIYGIIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHVLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120
DB 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
QY 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
DB 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337
DB 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337

RESULT 13

US-10-292-798-464

; Sequence 464, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 464
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-464

Query Match 100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPKMHVLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120
DB 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKEIRSFHFNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
QY 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
DB 181 SACDLTSSDELNTIKWYNLLTATTFCLPLVIVVTLVCTTIIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVVCFLPFLHVRIRIESRLLSISCSIEHQHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337
DB 301 LYVVSDNFQAVCVTRCKVSGNLEQAQKISYNNP 337

RESULT 14

US-10-023-634-6
; Sequence 6, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R

```
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-634-6

Query Match      100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0;

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Db 1 MNEPLDYLANASDFDYAAAFGCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKWSTIIMLNACTDLYLTSLPFLIHVYASGENWIFGDMCKFIRFSHFNLVSS 120
Db 61 KMRPKWSTIIMLNACTDLYLTSLPFLIHVYASGENWIFGDMCKFIRFSHFNLVSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWNLILTATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCLKQKAR 240
Db 181 SACLDTSSDELNTIKWNLILTATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCLKQKAR 240
QY 241 RLTILLALLAFYVCFPLPFHLIRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
Db 241 RLTILLALLAFYVCFPLPFHLIRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
QY 301 LVVVSDNFQQAVCSIVRCKVSGNLEQAKKISYNNP 337
Db 301 LVVVSDNFQQAVCSIVRCKVSGNLEQAKKISYNNP 337
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RESULT 15

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US-10-023-634-57
; Sequence 57, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
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; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-634-57

Query Match      100.0%; Score 1771; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e-156; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0;

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Db 1 MNEPLDYLANASDFDYAAAFGCNCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPKWSTIIMLNACTDLYLTSLPFLIHVYASGENWIFGDMCKFIRFSHFNLVSS 120
Db 61 KMRPKWSTIIMLNACTDLYLTSLPFLIHVYASGENWIFGDMCKFIRFSHFNLVSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWNLILTATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCLKQKAR 240
Db 181 SACLDTSSDELNTIKWNLILTATTFCLPLVIVTLCTYTTIIHTLTHGLQDSCLKQKAR 240
QY 241 RLTILLALLAFYVCFPLPFHLIRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
Db 241 RLTILLALLAFYVCFPLPFHLIRVIRIESRLSSCSIEHQIHEAYIVSRPLAINTFGNLL 300
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Db 241 RLTI LLLAFYVCF LPHLEVRIRIESRLLSISCS IENQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVVSDNFQOAVGCVTRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVVSDNFQOAVGCVTRCKVSGNLEQAKKISYNNP 337

Search completed: October 29, 2004, 15:07:49
Job time : 144 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2004, 14:13:22 ; Search time 159 Seconds
(without alignments)
760.326 Million cell updates/sec

Title: US-10-763-854-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANRDPDYAAA.....RCKVSGNLEQAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1771	100.0	337	4 AAU04375	Aau04375 Human G-p
2	1771	100.0	337	5 AAE16171	Aae16171 Human G-p
3	1771	100.0	337	5 ABG76871	Abg76871 Human G-p
4	1771	100.0	337	5 AB883819	Ab883819 Human P2Y
5	1771	100.0	337	5 ABG70271	Abg70271 Human Pur
6	1771	100.0	337	5 AAO14027	Aao14027 Human Pur
7	1771	100.0	337	5 AAU77600	Aau77600 Human P2Y
8	1771	100.0	337	5 AAE21803	Aae21803 Human AXO
9	1771	100.0	337	5 ABP95602	Abp95602 Human GPC
10	1771	100.0	337	5 AAO15399	Aao15399 Human G-p
11	1771	100.0	337	5 AB879438	Ab879438 Human P2Y
12	1771	100.0	337	5 AB881902	Ab881902 Human G-p
13	1771	100.0	337	5 ABG70287	Abg70287 Human nov
14	1771	100.0	337	6 ABP71377	Abp71377 Human TGR
15	1771	100.0	337	7 ADC26010	Adc26010 Human Pur
16	1771	100.0	337	7 ADC86011	Adc86011 Human GPC
17	1771	100.0	337	7 ABW00808	Abw00808 Human GPC
18	1771	100.0	337	7 ADL96474	Adl96474 Human G-p
19	1771	100.0	337	8 ADM10574	Adm10574 Human P2Y
20	1771	100.0	337	8 ADO29442	Ado29442 Human GPC
21	1771	100.0	337	6 AAE33315	Aae33315 Human TAR
22	1771	100.0	345	6 AAE33317	Aae33317 Human TAR
23	1771	100.0	363	6 AAE33318	Aae33318 Human TAR
24	1771	100.0	577	7 ADF70488	Adf70488 Orphan re
25	1764	99.6	337	4 AAU04584	Aau04584 Human G-p

ALIGNMENTS

RESULT 1

AAU04375

ID AAU04375 standard; protein; 337 AA.

XX AC AAU04375;

XX DT 23-OCT-2001 (first entry)

XX DE Human G-protein coupled receptor, hrUP21.

XX KW Human; G-protein coupled receptor; GPCR; hrUP21; agonist;

XX XW inverse agonist; lung cancer.

XX OS Homo sapiens.

XX PN WO200136471-A2.

XX PD 25-MAY-2001.

XX PF 16-NOV-2000; 2000WO-US031509.

XX PR 17-NOV-1999; 99US-0166088P.

XX PR 17-NOV-1999; 99US-0166099P.

XX PR 23-DEC-1999; 99US-0166369P.

XX PR 23-DEC-1999; 99US-0171900P.

XX PR 23-DEC-1999; 99US-0171901P.

XX PR 11-FEB-2000; 2000US-0181749P.

XX PR 14-MAR-2000; 2000US-0189259P.

XX PR 10-APR-2000; 2000US-0195898P.

XX PR 10-APR-2000; 2000US-0195899P.

XX PR 10-APR-2000; 2000US-0196078P.

XX PR 28-APR-2000; 2000US-0200419P.

XX PR 12-MAY-2000; 2000US-0203630P.

XX PR 12-JUN-2000; 2000US-0210741P.

XX PR 12-JUN-2000; 2000US-0210982P.

XX PR 21-AUG-2000; 2000US-0226760P.

XX PR 26-SEP-2000; 2000US-0235418P.

XX PR 26-SEP-2000; 2000US-0235779P.

XX PR 20-OCT-2000; 2000US-0242332P.

XX PR 20-OCT-2000; 2000US-0242343P.

XX PR 24-OCT-2000; 2000US-0243019P.

XX (AREN-) ARENA PHARM INC.

XX PA Chen R, Dang HT, Lowitz KP;

XX PI

XX XX

Abp81736 Human G p
Adh68217 Human G-p
Adc25998 Human Pur
Aag80971 Human nGP
Abg93789 Human G p
Adc12674 Human GPC
Adm10576 Murine P2
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Aae33316 Mouse TAR
Adm10578 Rat P2Y25
Ab883818 Human P2Y
Aam79297 Human pro
Abd11082 Human P2Y
Aam80281 Human pro
Aag80958 Human nGP
Abg93776 Human G p
Adf43212 Mouse P2R
Ado29593 Mouse GPC
Aae04389 Human P2-
Abp54316 Human P2Y

DR WPI; 2001-355616/37.
 DR N-PSDB; AAS07948.
 XX Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents.
 XX
 PS Claim 53; Page 114-115; 160pp; English.
 CC
 CC The sequence represents a human G-protein coupled receptor (GPCR),
 CC hRUP21. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer. Non-
 CC endogenous version of human GPCRs are also utilized in research settings
 CC and in vitro and in vivo system, incorporating GPCRs can be utilised to
 CC elucidate and understand the roles these receptors play in the human
 CC condition, both normal and diseased
 XX
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1771; DB 4; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIRSFHNLSS 120
 DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIRSFHNLSS 120
 QY 121 ILFLTCSIFRYCVIIHPMSCFHSIKTKCAVAVVWIIISLVAVIPMTFLTSTNTR 180
 DB 121 ILFLTCSIFRYCVIIHPMSCFHSIKTKCAVAVVWIIISLVAVIPMTFLTSTNTR 180
 QY 181 SACLDTSSDELNTIKWNLILITATTCFLPLVITVLCVYTIHITLHGLQDSCCLKOKAR 240
 DB 181 SACLDTSSDELNTIKWNLILITATTCFLPLVITVLCVYTIHITLHGLQDSCCLKOKAR 240
 QY 241 RLTIILLAFVYCFPLPHILVIRIESRLLSISCSIQENQHEAVIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFVYCFPLPHILVIRIESRLLSISCSIQENQHEAVIVSRPLAALNTFGNLL 300
 QY 301 LYVVSDNFQAVCVSTVECKVSGNLEQAKKISYNNP 337
 DB 301 LYVVSDNFQAVCVSTVECKVSGNLEQAKKISYNNP 337
 RESULT 2
 AAEL16171
 ID AAEL16171 standard; protein; 337 AA.
 XX
 AC AAEL16171;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 XX Human G-protein coupled receptor 2 (GCR2-2) protein.
 XX
 KW Human; G-protein coupled receptor 2; cell proliferative disorder;
 KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
 KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
 KW acquired immune deficiency syndrome; inflammatory disorder; infection;
 KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
 KW diabetes; obesity; osteoporosis; gene therapy; GCR2-2.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

FT Domain 35. .59
 FT /note= "Transmembrane domain"
 XX
 XX WO200187937-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 17-MAY-2001; 2001WO-US016285.
 XX
 XX 18-MAY-2000; 2000US-0205628P.
 XX 22-MAY-2000; 2000US-0206222P.
 XX 25-MAY-2000; 2000US-0207566P.
 XX 02-JUN-2000; 2000US-0208834P.
 XX 02-JUN-2000; 2000US-0208861P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, Graul R;
 XX Khan FA, Gandhi AR, Wallia NK, Nguyen DB, Yue H, Hafalia A;
 XX Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;
 XX
 XX WPI; 2002-089844/12.
 XX N-PSDB; AAD26370.
 DR
 DR Novel G-protein coupled receptors and polynucleotides useful for
 PT diagnosis, treatment and prevention of disorders of cell proliferation,
 PT neurological, cardiovascular, metabolic disorders and viral infections.
 XX
 XX Claim 1; Page 104-105; 115pp; English.
 XX
 XX The invention relates to human G-protein coupled receptor (GCR2)
 CC polypeptides and polynucleotides. GCR2 polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in the
 CC diagnosis, prevention and treatment of disorders which include cell
 CC proliferative disorders such as arteriosclerosis, hepatitis,
 CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
 CC lymphoma; neurological disorders such as epilepsy, ischaemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerotic heart
 CC hypertension, vascular tumours, myocardial infarction, hypertensive heart
 CC disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and viral
 CC infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are
 CC also used as probes for assessing toxicity of test compounds. They are also
 CC used in gene therapy. The present sequence is human G-protein coupled
 CC receptor 2 (GCR2-2) protein
 XX
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1771; DB 5; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 QY 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIRSFHNLSS 120
 DB 61 KMRPWKSTIIIMNLACTDLYLTLSPFLIHYYASGENWIFGDFMCKFIRSFHNLSS 120

QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
QY 181 SACDLTSSDELTNTIKWYNLILTATFTFCLPLVIVTLCTTTIHTLTHGLQDSCCLKQKAR 240
DB 181 SACDLTSSDELTNTIKWYNLILTATFTFCLPLVIVTLCTTTIHTLTHGLQDSCCLKQKAR 240
QY 241 RLTLILLAFVVCFLPHILRVIRIESLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTLILLAFVVCFLPHILRVIRIESLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 3

ABG76871
ID ABG76871 standard; protein; 337 AA.

XX AC ABG76871;

DT 05-NOV-2002 (first entry)

XX DE Human G-protein coupled receptor, HGPRBMV23.

XX KW Human; G-protein coupled receptor; HGPRBMV23; receptor; GPCR; cancer;
KW renal disorder; pulmonary disease; neural disorder; heart defect;
KW male reproductive disorder; hyperproliferative disorder; inflammation;
KW lymphoproliferative disease; autoimmune disease; bacterial infection;
KW fungal infection; parasitic infection; vascular disorder; receptor;
KW lymphatic disorder.

XX OS Homo sapiens.

XX PN WO200246414-A2.

XX PD 13-JUN-2002.

XX PF 07-DEC-2001; 2001WO-US046951.

XX PR 07-DEC-2000; 2000US-0251926P.

XX PR 14-FEB-2001; 2001US-0265795P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Ramanathan C, Feder J, Nelson T, Cacace A, Barber L, Rysek R;

XX DR WPI; 2002-599468/64.

XX DR N-PSDB; ABS59232.

XX PT New G-protein coupled receptor HGPRBMV23 polypeptide and polynucleotides,
PT useful for diagnosing, prognosing, preventing, treating renal, immune,
PT hyperproliferative and cardiovascular disorders and identifying
PT modulators.

XX PS Claim 33; Fig 1; 419pp; English.

XX CC The invention relates to an isolated G-protein coupled receptor (GPCR)
CC protein, HGPRBMV23. The protein and its associated DNA are useful for
CC preventing, treating or ameliorating a medical condition such as a renal
CC disorder, a disorder associated with pulmonary disease (e.g. chronic
CC obstructive pulmonary disease, cystic fibrosis, pulmonary thrombosis),
CC neural disorders (e.g. Alzheimer's disease, Parkinson's disease,
CC depression, psychoses), male reproductive disorders (e.g. male
CC infertility, impotence, testicular cancer), heart defects (e.g.
CC endocardial cushion defects, arrhythmia, myocardial ischaemia, myocardial
CC infarction, pericardial effusion), hyperproliferative disorders,
CC lymphoproliferative diseases; autoimmune disease (e.g. Addison's disease,
CC multiple sclerosis, ophthalmia, diabetes mellitus), cancer, inflammation
CC (e.g. graft versus host disease, chronic graft rejection), bacterial,
CC fungal or parasitic infection (e.g. bacteraemia, endocarditis, whooping

CC cough, sepsis, food poisoning, pneumonia, wound infection, dysentery),
CC vascular disorders and lymphatic disorders. This sequence represents the
CC human HGPRBMV23 polypeptide

XX SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.le-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDVAAPGNCNTDENIPDKMHLVPVIYGIIFLVGPGNAVISTYIF 60

DB 1 MNEPLDYLANASDPDVAAPGNCNTDENIPDKMHLVPVIYGIIFLVGPGNAVISTYIF 60

QY 61 KMRPWKSTIIMLNACTDLYLTSLPDLHYASGENWIFGDFMCKFIRSEHFNLSS 120

DB 61 KMRPWKSTIIMLNACTDLYLTSLPDLHYASGENWIFGDFMCKFIRSEHFNLSS 120

QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180

DB 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180

QY 181 SACDLTSSDELTNTIKWYNLILTATFTFCLPLVIVTLCTTTIHTLTHGLQDSCCLKQKAR 240

DB 181 SACDLTSSDELTNTIKWYNLILTATFTFCLPLVIVTLCTTTIHTLTHGLQDSCCLKQKAR 240

QY 241 RLTLILLAFVVCFLPHILRVIRIESLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300

DB 241 RLTLILLAFVVCFLPHILRVIRIESLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300

QY 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYSNNP 337

DB 301 LYVVSDNFQAVGVSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 4

ABB83819
ID ABB83819 standard; protein; 337 AA.

XX AC ABB83819;

XX DT 18-SEP-2002 (first entry)

XX DE Human P2Y-like receptor variant SEQ ID NO 4.

XX KW Human; P2Y-like receptor; HIPHUM 0000037; immunity; inflammation; cancer;
KW Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
KW immunomodulator; anti-inflammatory; cytostatic; antisthmatic;
KW gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;
KW antibacterial; immunosuppressive; dermatological; nephrotropic;
KW antiallergic; analgesic; receptor.

XX OS Homo sapiens.

XX PN GB2369364-A.

XX PD 29-MAY-2002.

XX PF 31-AUG-2001; 2001GB-00021215.

XX PR 01-SEP-2000; 2000GB-00021524.

XX PR 06-SEP-2000; 2000GB-00021894.

XX PR 25-SEP-2000; 2000GB-00023444.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Foord SM, Ignar DM;

XX DR WPI; 2002-511268/55.

XX DR N-PSDB; ABN85630.

XX PT An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be
PT used for the identification of agonists and antagonists which may be used

to treat an immune or inflammatory disease.

Claim 1; Page 30-31; 35pp; English.

The invention relates to an isolated P2Y-like receptor polypeptide (ABB83818-ABB83819) which is also referred to in the specification as HIPHUM 000037. An effective amount of a substance (agonist or antagonist) which modulates P2Y receptor activity is useful to treat a subject having a disorder that is responsive to P2Y-like receptor modulation. The disorder is a disease of immunity or inflammation. The substance may also be used to manufacture a medicine for the treatment or prophylaxis of a disorder that is responsive to stimulation or modulation of P2Y-like receptor activity. Disorders which may be treated include colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome, gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative colitis, rheumatoid arthritis, viral diseases, bacterial infections, autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic rhinitis, inflammatory pain and general inflammation such as tendonitis, polymyositis or prostatitis. The invention provides alternative CC substances for the treatment of immunological and inflammatory diseases

XX Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.1e-194;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPDKMHLVPIYGIIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPDKMHLVPIYGIIFLVGPGNAVISTYIF 60
QY 61 KMRPWKSTIIMNLACTDLIYLSPLPIHYASGENWIFGDFWCKFIRESFHNLYSS 120
DB 61 KMRPWKSTIIMNLACTDLIYLSPLPIHYASGENWIFGDFWCKFIRESFHNLYSS 120
QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWVMSILVAVIPMTFLITSTNTR 180
DB 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWVMSILVAVIPMTFLITSTNTR 180
QY 181 SACLIDLTSSDLNTIKWNLITLTATPCPLPIVITVLCVTTIHTLTGLQDSCCLKQKAR 240
DB 181 SACLIDLTSSDLNTIKWNLITLTATPCPLPIVITVLCVTTIHTLTGLQDSCCLKQKAR 240
QY 241 RLTIILLAFYVCFPLPHILVRISERLLSISCIENQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFYVCFPLPHILVRISERLLSISCIENQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVTRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQAVCVTRCKVSGNLEQAKKISYNNP 337

RESULT 5

ABG70271

ID ABG70271 standard; protein; 337 AA.

XX AC ABG70271;

XX DT 05-NOV-2002 (first entry)

XX DE Human Purinoceptor-like protein.

XX Human; NOXV; pathological condition; NOXV-associated disorder;
KW Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
KW pancreatitis; obesity; diabetes; autoimmune disease; infertility;
KW renal artery stenosis; interstitial nephritis; glomerulonephritis;
KW polycystic kidney disease; cataract; Alzheimer's disease; cancer;
KW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
KW congenital heart defect; scleroderma; endometriosis; haemophilia;
KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
KW acne; wound; asthma; human disease; calpain; epsin; zinc finger;
KW low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;

KW

KW serine protease TLSP; mitogen activated protein kinase kinase-2;

XX glypican-2 precursor; thymosin beta-10.

OS Homo sapiens.

XX WO200255702-A2.

XX 18-JUL-2002.

XX 26-OCT-2001; 2001WO-US050925.

XX 26-OCT-2000; 2000US-0243320P.

XX 26-OCT-2000; 2000US-0243592P.

XX 26-OCT-2000; 2000US-0243642P.

XX 27-OCT-2000; 2000US-0243681P.

XX 27-OCT-2000; 2000US-0243863P.

XX 31-OCT-2000; 2000US-0244443P.

XX 01-NOV-2000; 2000US-0244995P.

XX 01-NOV-2000; 2000US-0245029P.

XX 02-NOV-2000; 2000US-0245293P.

XX 02-NOV-2000; 2000US-0245315P.

XX 02-NOV-2000; 2000US-0245316P.

XX 19-JAN-2001; 2001US-0262994P.

XX 15-FEB-2001; 2001US-02629056P.

XX 02-MAR-2001; 2001US-0272923P.

XX 15-MAR-2001; 2001US-0276565P.

XX 07-SEP-2001; 2001US-0318119P.

XX (CURA-) CURAGEN CORP.

PI Gangolli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L;

PI Vernet CAM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;

PI Malyankar U, Stone D, Millet I, Smithson G, Gunther E, Padigaru M;

PI Taupier RJ, Anderson D;

XX WPI; 2002-590673/63.

DR N-PSDB; ABK51678.

XX Isolated NOXV polypeptides and nucleic acid molecules useful for treating, preventing, diagnosing and researching pathological conditions in humans with a NOXV-associated disorders, e.g. cancer, stroke or Alzheimer's disease.

XX Claim 1; Page 32; 236pp; English.

XX The present invention relates to a new polypeptide that comprises any of 17 fully defined sequences of 43-990 amino acids given in the specification. The NOXV polypeptide, nucleic acid and antibody of the invention are useful for treating or preventing a pathological condition in humans with a NOXV-associated disorder, e.g. Von Hippel-Lindau syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity, diabetes, autoimmune disease, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, cataract, Alzheimer's disease, acoustic trauma, cancer, infertility, cardiomyopathies, atherosclerosis, hypertension, congenital heart defects, scleroderma, endometriosis, haemophilia, dementia, stroke, Parkinson's disease, Huntington's disease, epilepsy, multiple sclerosis, anxiety, pain, leukaemia, hypothyroidism, psoriasis, acne, wounds and asthma. They are also useful for the manufacture of a medicament for treating a syndrome associated with a human disease, specifically a NOXV-associated disorder. They may also be useful in therapeutic applications including protein therapy, as small molecule drug targets, as antibody targets, as diagnostic and/or prognostic markers, in gene therapy, as research tools and in tissue regeneration. The present amino acid sequence represents one of the 17 novel proteins of the invention

XX Sequence 337 AA;

Query Match

Best Local Similarity 100.0%; Score 1771; DB 5; Length 337;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPDKMHLVPIYGIIFLVGPGNAVISTYIF 60

```
|||||
1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHVLPVIYGLIFLVGPGNAVISTYIF 60
61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIKFSFHNLYSS 120
61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIKFSFHNLYSS 120
121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVMIISLVAIPMTFLTITSTNTR 180
121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVMIISLVAIPMTFLTITSTNTR 180
181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCVTTIIHTLHGLQDSCLKQAR 240
181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCVTTIIHTLHGLQDSCLKQAR 240
241 RLTIILLAFYVCFPLPHILVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
241 RLTIILLAFYVCFPLPHILVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
301 LYVVSDNFQAVCVTVCKVSGNLEQAKKISYSNNP 337
301 LYVVSDNFQAVCVTVCKVSGNLEQAKKISYSNNP 337

RESULT 6
AAO14027
ID AAO14027 standard; protein; 337 AA.
XX AAO14027;
AC AAO14027;
XX
DT 30-APR-2002 (first entry)
DE Human purinergic-related G-protein coupled receptor (GPCR).
XX
KW Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
KW signal transduction; human protease; GPCR disorder; gene therapy;
KW transgenic animal; receptor.
XX
OS Homo sapiens.
XX
PN WO200187980-A2.
XX
PD 22-NOV-2001.
XX
PF 17-MAY-2001; 2001WO-US015957.
XX
PR 18-MAY-2000; 2000US-0205196P.
XX
PR 08-AUG-2000; 2000US-00634656.
XX
PA (APPL-) APPLERA CORP.
XX
PI Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
XX
DR WPI; 2002-075312/10.
XX
DR N-PSDB; AAK98323, AAK98324.
XX
PT Novel isolated G-protein coupled receptor peptide useful for treating
PT disorder characterized by absence of, in appropriate or unwanted
PT expression of the receptor protein, and as immunogens to raise
PT antibodies.
XX
PS Claim 1; Fig 2; 64pp; English.
XX
CC The present specifically claimed sequence represents a human purinergic-
CC related G-protein coupled receptor (GPCR) encoded by a gene on chromosome
CC 13. GPCRs constitute a major class of proteins responsible for signal
CC transduction within a cell. Upon binding of a ligand to the extracellular
CC portion of a GPCR, a signal is transduced resulting in a biological or
CC physiological change within the cell. The GPCR proteins can be divided
CC into five families, family I contains the purinergic GPCRs (e.g. the P2Y
CC receptors). P2Y receptors are characterised by their selective
CC responsiveness towards ATP and its analogues, some also respond to UTP.
CC The invention comprises a human G-protein coupled receptor protein and
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CC encoding nucleic acids. The GPCR protein and nucleic acids of the
CC invention are useful in the treatment of a disease or condition mediated
CC by a human protease. The GPCR protein of the invention is useful for: the
CC development/identification of therapeutic proteins; assays designed to
CC quantitatively determine levels of the protein in biological fluids;
CC identifying compounds which modulate the activity of the GPCR, or the
CC interaction of the GPCR and a molecule with which it normally interacts;
CC and treating a disorder characterised by an absence of, or inappropriate
CC expression of the GPCR protein. The GPCR nucleic acids of the invention
CC are useful in diagnostic assays to identify changes in the GPCR nucleic
CC acid that lead to pathology; controlling GPCR expression; and in gene
CC therapy to treat patients with aberrant GPCR gene expression. The GPCR
CC nucleic acids can also be used in the production of transgenic animals
XX
SQ Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHVLPVIYGLIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCTDENIPLKMHVLPVIYGLIFLVGPGNAVISTYIF 60
QY 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIKFSFHNLYSS 120
DB 61 KMRPWKSTIIMNLACTDLYLTLSPFLIHVYASGENWIFGDFMCKFIKFSFHNLYSS 120
QY 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVMIISLVAIPMTFLTITSTNTR 180
DB 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVMIISLVAIPMTFLTITSTNTR 180
QY 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCVTTIIHTLHGLQDSCLKQAR 240
DB 181 SACLDTSSDELNTIKWNLILTATTCFLPLVIVTLCVTTIIHTLHGLQDSCLKQAR 240
QY 241 RLTIILLAFYVCFPLPHILVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFYVCFPLPHILVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCVTVCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVSDNFQAVCVTVCKVSGNLEQAKKISYSNNP 337

RESULT 7
AAU77600
ID AAU77600 standard; protein; 337 AA.
XX AAU77600;
AC AAU77600;
XX
DT 05-JUN-2002 (first entry)
DE Human P2Y1-like G protein-coupled receptor.
XX
KW Human; P2Y1-like G protein-coupled; receptor; GPCR; infection; pain;
KW cancer; anorexia; bulimia; asthma; hypotension;
KW central nervous system disease; acute heart failure; hypertension;
KW urinary retention; osteoporosis; diabetes; angina pectoris;
KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
KW benign prostatic hypertrophy; psychosis; neurological disorder;
KW dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
KW dementia; severe mental retardation; Huntington's disease;
KW Tourette's syndrome.
XX
OS Homo sapiens.
XX
PN WO200214511-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-EP009243.
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XX PR 14-AUG-2000; 2000US-0224989P.
XX PA (FARB ) BAYER AG.
XX PI Ramakrishnan S;
XX DR WPI; 2002-257607/30.
XX DR N-PSDB; ABK11381.
XX PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can be
XX PT regulated for treating infection, pain, cancer, diabetes, anorexia,
XX PT asthma, hypertension, neurological disorder and dyskinesia.
XX PS Claim 25; Fig 2; 118pp; English.
XX CC The invention relates to a purified human P2Y1-like G protein-coupled
XX CC receptor (GPCR) polypeptide and the nucleic acids encoding it (including
XX CC 5' and 3' sequences, promoters, fragments, variants, or a sequence
XX CC encoding a protein at least 50% identical to the GPCR). Also included are
XX CC an expression vector comprising the nucleic acid, a host cell containing
XX CC the vector and the identification of modulators of the GPCR especially
XX CC those that reduce the activity of the GPCR. The nucleic acid is useful
XX CC for detecting a polynucleotide encoding the GPCR in a biological sample.
XX CC The GPCR and nucleic acid are useful for screening for agents which
XX CC decrease the activity of the GPCR and for modulators of the GPCR. The
XX CC modulator or agent useful for modulating the activity of P2Y1-like G
XX CC protein-coupled receptor in a disease such as bacterial, fungal,
XX CC protozoan, and viral infection, pain, cancer, anorexia, bulimia, asthma,
XX CC central nervous system (CNS) disease, acute heart failure, hypertension,
XX CC hyperextension, urinary retention, osteoporosis, diabetes, angina pectoris,
XX CC myocardial infarction, ulcer, inflammation, allergy, multiple sclerosis,
XX CC benign prostatic hypertrophy, psychotic and neurological disorders,
XX CC dyskinesias, HIV virus infection (human immunodeficiency virus), CNS
XX CC disorders such as Parkinson's disease, anxiety, schizophrenia, manic
XX CC depression, delirium, dementia, severe mental retardation, Huntington's
XX CC disease and Tourette's syndrome. The present sequence represents the P2Y1
XX CC -like GPCR of the invention
XX SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGLIPLVGPFGNAVISTYIF 60
DB 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGLIPLVGPFGNAVISTYIF 60
QY 61 KMRPWKSTIIIMNLACTDLYLTSPLFIHYHYPGENWIFGDFMCKFIKFSHFNLVSS 120
DB 61 KMRPWKSTIIIMNLACTDLYLTSPLFIHYHYPGENWIFGDFMCKFIKFSHFNLVSS 120
QY 121 ILELTCFSIFRYCVIIHPMSCFSIHKTCAVAVCAVAVVWIIISLVAVIPMTLITSTNTR 180
DB 121 ILELTCFSIFRYCVIIHPMSCFSIHKTCAVAVCAVAVVWIIISLVAVIPMTLITSTNTR 180
QY 181 SACLDTSSDEINTIKWNLIIITATTCFLPVIVTLCTVITIIHTLTHGLQDSCILKQAR 240
DB 181 SACLDTSSDEINTIKWNLIIITATTCFLPVIVTLCTVITIIHTLTHGLQDSCILKQAR 240
QY 241 RLTIILLAFVCFPLPHILRVIRIESRLISCSIQENQIHEAVIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFVCFPLPHILRVIRIESRLISCSIQENQIHEAVIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQAVCSITVRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQAVCSITVRCKVSGNLEQAKKISYNNP 337

RESULT 8
1. AAE21803
ID AAE21803 standard; protein; 337 AA.

```

```

XX AC AAE21803;
XX DT 16-JUL-2002 (first entry)
XX DE Human AXOR89 (G-protein coupled receptor) protein.
XX KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
XX KW infection; cancer; pain; asthma; Parkinson's disease; diabetes; obesity;
XX KW anorexia; bulimia; acute heart failure; hypertension; hypertension; ulcer;
XX KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
XX KW myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
XX KW vomiting; psychotic; neurological disorder; anxiety; manic depression;
XX KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;
XX KW dementia; dyskinesia.
XX OS Homo sapiens.
XX FN GB2365012-A.
XX PD 13-FEB-2002.
XX PF 10-MAY-2001; 2001GB-00011437.
XX PR 11-MAY-2000; 2000US-00569137.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Elshourbagy N, Shabon U;
XX WPI; 2002-332558/37.
XX N-PSDB; AAD34278.
XX PT Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
XX PT identifying agonists and antagonists in the treatment of diseases
XX PT associated with an AXOR89 imbalance, such as cancers, diabetes or asthma.
XX PS Claim 1; Page 30; 37pp; English.
XX CC The invention relates to an isolated AXOR89 polypeptide (G-protein
XX CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
XX CC and polynucleotide encoding the polypeptide, is useful for identifying
XX CC agonists and antagonists (or inhibitors) that are potentially useful in
XX CC treating conditions associated with an AXOR89 imbalance, such as
XX CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
XX CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
XX CC failure, hypertension, hyperextension, urinary retention, osteoporosis,
XX CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
XX CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
XX CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
XX CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
XX CC syndrome. The polynucleotide sequence may also be used for chromosome
XX CC localisation or tissue expression studies. The AXOR89 is used as a
XX CC vaccine or to produce fusion proteins. The present sequence is human
XX CC AXOR89 protein
XX SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGLIPLVGPFGNAVISTYIF 60
DB 1 MNEPLDYLANASDFPDYAAAFNGCTDENIPLKMHYLPVIYGLIPLVGPFGNAVISTYIF 60
QY 61 KMRPWKSTIIIMNLACTDLYLTSPLFIHYHYPGENWIFGDFMCKFIKFSHFNLVSS 120
DB 61 KMRPWKSTIIIMNLACTDLYLTSPLFIHYHYPGENWIFGDFMCKFIKFSHFNLVSS 120
QY 121 ILELTCFSIFRYCVIIHPMSCFSIHKTCAVAVCAVAVVWIIISLVAVIPMTLITSTNTR 180
DB 121 ILELTCFSIFRYCVIIHPMSCFSIHKTCAVAVCAVAVVWIIISLVAVIPMTLITSTNTR 180

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Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWYNLIITATTCFLPLVITLCYTTIIHTLTHGLQTSCLKQKAR 240
Db 181 SACLDTSSDELNTIKWYNLIITATTCFLPLVITLCYTTIIHTLTHGLQTSCLKQKAR 240
QY 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Db 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
RESULT 9
ID ABP95602 standard; protein; 337 AA.
AC ABP95602;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polypeptide SEQ ID NO 14.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
XX
DR N-PSDB; AB242876.
XX
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 10; SEQ ID NO 14; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDFPDYAAAFGNCNTDENIPLKMHYLPVIYGIIFLVGFGNNAVISTYIF 60
|||||

Db 1 MNEPLDYLANASDFPDYAAAFGNCNTDENIPLKMHYLPVIYGIIFLVGFGNNAVISTYIF 60
QY 61 KMRPKWSTIIMNLACTDLYLTSLPFLIHVYASGENWIFGDMCKFRFSPHENLYSS 120
Db 61 KMRPKWSTIIMNLACTDLYLTSLPFLIHVYASGENWIFGDMCKFRFSPHENLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVACAVVWIIISLVAVIPMTFLTITSTNRTNR 180
QY 181 SACLDTSSDELNTIKWYNLIITATTCFLPLVITLCYTTIIHTLTHGLQTSCLKQKAR 240
Db 181 SACLDTSSDELNTIKWYNLIITATTCFLPLVITLCYTTIIHTLTHGLQTSCLKQKAR 240
QY 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
Db 241 RTILLALLAFYVCFPLPHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
Db 301 LYVVVSDNFQAVCVSTVRCKVSGNLEQAKKISYNNP 337
RESULT 10
ID AAO15399 standard; protein; 337 AA.
XX
AC AAO15399;
XX
DT 27-SEP-2002 (first entry)
XX
DE Human G protein-coupled receptor.
XX
KW Human; gene therapy; G protein-coupled receptor; drug development;
KW central nervous system disease; endocrine disease; metabolic disease;
KW cancer; respiratory disease; digestive disease; immune disease;
KW inflammation; infection; circulatory disease.
XX
OS Homo sapiens.
XX
PN WO200257441-A1.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-JP000270.
XX
PR 18-JAN-2001; 2001JP-00010714.
PR 30-MAR-2001; 2001JP-00102484.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Miwa M, Ito T, Shintani Y, Miyajima N;
XX
DR WPI; 2002-566800/60.
XX
DR N-PSDB; AAL43942.
XX
PT Human kidney-originated G protein-coupled receptor protein TGR30 and
PT encoded DNA, for developing drugs to treat central nervous diseases,
PT endocrine diseases, metabolic diseases and cancer, including gene
PT therapy.
XX
PS Claim 1; Page 88-90; 98pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequence of a human G
CC protein-coupled receptor. The DNA and protein sequences of the invention
CC are useful for developing drugs to prevent or treat (gene therapy):
CC central nervous system diseases; endocrine diseases; metabolic diseases;
CC cancer; respiratory diseases; digestive diseases; immune diseases;
CC inflammations; infections; and circulatory diseases. The present amino
CC acid sequence represents the human G protein-coupled receptor of the
CC invention
XX
SQ Sequence 337 AA;

```
Query Match      100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
QY 61 KMRPKWSTIIIMNLACTDLYLTSPLPELIHYASGENWIFGDFMCKEIRSFHFNLYSS 120
DB 61 KMRPKWSTIIIMNLACTDLYLTSPLPELIHYASGENWIFGDFMCKEIRSFHFNLYSS 120
QY 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAIPMTFLTITSTNRTNR 180
DB 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAIPMTFLTITSTNRTNR 180
QY 181 SACLDLTSSDELNTIKWNLILTATTCFLPLVIVTLCVYTTIIHTLTHGLQDSCCLKOKAR 240
DB 181 SACLDLTSSDELNTIKWNLILTATTCFLPLVIVTLCVYTTIIHTLTHGLQDSCCLKOKAR 240
QY 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 11
ABB79438
ID ABB79438 standard; protein; 337 AA.
AC ABB79438;
XX
DT 05-JUL-2002 (first entry)
DE Human P2Y1-1i.
KW Human; P2Y1-1i; G protein-coupled; receptor; gene therapy; thyroid.
OS Homo sapiens.
XX
FN DE10046970-A1.
XX
PD 11-APR-2002.
XX
PF 22-SEP-2000; 2000DE-01046970.
XX
PR 22-SEP-2000; 2000DE-01046970.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
DR WPI; 2002-353329/39.
XX
N-PSDB; ABL56197.
XX
PT New human P2Y1li gene, useful for treatment and diagnosis of associated
PT diseases, and related proteins, antibodies and modulators, encodes G
PT protein-coupled receptor.
XX
PS Claim 4; Page 3; 5pp; German.
XX
CC The invention relates to the human P2Y1li gene (I), including its 5' and
CC 3' untranslated regions, located on chromosome 13 and encoding a G
CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
CC etc., are used for diagnosis and (gene) therapy of diseases that are
CC (in)directly associated with (I) or its expression products. No diseases
CC are specified but as (I) is expressed only in thyroid tissue, (I) is
CC presumed to be involved in regulation of thyroid function. The present
```

```
CC sequence is that of P2Y1li
SQ Sequence 337 AA;
Query Match      100.0%; Score 1771; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
DB 1 MNEPLDYLANASDPDYAAAFNGCTDENIPKMHYLPVIYGIIFLVGPGNAVISTVIF 60
QY 61 KMRPKWSTIIIMNLACTDLYLTSPLPELIHYASGENWIFGDFMCKEIRSFHFNLYSS 120
DB 61 KMRPKWSTIIIMNLACTDLYLTSPLPELIHYASGENWIFGDFMCKEIRSFHFNLYSS 120
QY 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAIPMTFLTITSTNRTNR 180
DB 121 ILFTCFISIFRYCVIIHPMCSFCSHKTRCAVAVCAVAVWIIISLVAIPMTFLTITSTNRTNR 180
QY 181 SACLDLTSSDELNTIKWNLILTATTCFLPLVIVTLCVYTTIIHTLTHGLQDSCCLKOKAR 240
DB 181 SACLDLTSSDELNTIKWNLILTATTCFLPLVIVTLCVYTTIIHTLTHGLQDSCCLKOKAR 240
QY 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
DB 241 RLTIILLAFYVCFPLPHILRVIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
QY 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVSDNFQOAVCVSTVRCKVSGNLEQAKKISYNNP 337

RESULT 12
ABB81902
ID ABB81902 standard; protein; 337 AA.
XX
AC ABB81902;
XX
DT 04-OCT-2002 (first entry)
DE Human G-protein coupled receptor PFI-019.
XX
KW Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
KW anti-inflammatory; cytostatic; cardiovascular; antiallergic; hypotensive;
KW antiarteriosclerotic; osteopathic; hypertension; asthma;
KW arteriosclerosis.
XX
OS Homo sapiens.
XX
PN EP1219638-A2.
XX
PD 03-JUL-2002.
XX
PF 04-DEC-2001; 2001EP-00310136.
XX
PR 18-DEC-2000; 2000GB-00030854.
XX
PR 04-MAY-2001; 2001GB-00011031.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Fidock MD;
XX
WPI; 2002-521945/56.
XX
N-PSDB; ABQ78847.
XX
PT New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y
PT purinoreceptor, useful for treating e.g. inflammation or cancers in a
PT patient, or for screening GPCR agonists or antagonists for treating these
PT diseases.
XX
PS Claim 11; Fig 2; 19pp; English.
```

XX The invention relates to a novel G-protein coupled receptor (GPCR), and
 CC the polynucleotide encoding it. The protein of the invention has
 CC neuroprotective, anti-inflammatory, cytotstatic, cardiovascular,
 CC anti-allergic, hypotensive, anti-arteriosclerotic, and osteopathic
 CC activity. The GPCR polypeptide is useful for manufacturing a medicament
 CC for treating a patient who needs to upregulate a receptor. Preferably,
 CC therapeutically useful areas are hypertension, asthma, and
 CC arteriosclerosis. The sequence represents the G-protein coupled receptor
 CC of the invention, PFI-019
 XX
 SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.le-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTVIF 60

Qy 61 KMRPKSSTIIMLNACTDILYLSLPPLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
 Db 61 KMRPKSSTIIMLNACTDILYLSLPPLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120

Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
 Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180

Qy 181 SACLDTSSDELNTIKWNLLITATTFCPLVIVTVLCVTTIHTLTHGLQDSCILKQKAR 240
 Db 181 SACLDTSSDELNTIKWNLLITATTFCPLVIVTVLCVTTIHTLTHGLQDSCILKQKAR 240

Qy 241 RLTIILLAFVVCFLPFIHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 Db 241 RLTIILLAFVVCFLPFIHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300

Qy 301 LYVVSDNFQAVGSTVRCKVSGNLEQAKKISYNNP 337
 Db 301 LYVVSDNFQAVGSTVRCKVSGNLEQAKKISYNNP 337

RESULT 13
 ABG70287
 ID ABG70287 standard; protein; 337 AA.

XX ABG70287;
 AC ABG70287;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human novel polypeptide #3.
 XX
 KW Human; trauma; viral infection; parasitic infection; addiction;
 KW bacterial infection; Alzheimer's disease; Huntington's disease; anxiety;
 KW Parkinson's disease; behavioural disorder; pain; hair growth disease;
 KW alopecia; pigmentation disorder; inflammatory disorder; arthritis; AIDS;
 KW inflammatory bowel disease; Crohn's disease; cancer; adenocarcinoma;
 KW acquired immunodeficiency syndrome; colon; asthma; hypertension; obesity;
 KW autoimmune disease; diabetes; graft versus host disease; ulcer; bulimia;
 KW anorexia; dementia; gene therapy.

OS Homo sapiens.
 XX
 PN WO200257452-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 17-DEC-2001; 2001WO-US049122.
 XX
 PR 15-DEC-2000; 2000US-0256025P.
 PR 30-JAN-2001; 2001US-0265163P.
 PR 02-MAR-2001; 2001US-0272929P.
 PR 09-MAR-2001; 2001US-0274864P.

PR 16-MAR-2001; 2001US-0276688P.
 PR 22-MAR-2001; 2001US-0277880P.
 PR 25-APR-2001; 2001US-0286409P.
 PR 31-JUL-2001; 2001US-0309246P.
 PR 29-AUG-2001; 2001US-0315600P.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RT, Colman SD, Spytek KA, Ballinger RA, Guo X;
 PI Tchernev VT, Shenoy SG, Li L, Ellerman KE, Zerhusen BD;
 PI Patturajan M, Casman SJ, Boldog F, Gusev VY, Burgess CE, Edinger S;
 PI Gangolli EA, Malyankar UM, Gunther E, Smithson G, Millet I;
 PI Gerlach VL;
 XX WPI: 2002-590743/63.
 DR N-PSDB; ABS51730.
 XX Novel polypeptide, designated NOVX for treating or preventing disorders
 PT or symptoms e.g. trauma, Alzheimer's disease, cancers, acquired
 PT immunodeficiency syndrome, asthma and rheumatoid arthritis.
 XX Claim 1; Page 25; 252pp; English.

PS The invention relates to human novel polynucleotides and polypeptides.
 XX The sequences are useful for the treatment, prevention and diagnosis of
 CC disorders such as trauma, viral/parasitic/bacterial infections,
 CC Alzheimer's disease, Huntington's disease, Parkinson's disease,
 CC behavioural disorders, anxiety, addiction, pain, hair growth diseases,
 CC alopecia, pigmentation disorder, inflammatory disorders such as osteo-
 CC and rheumatoid arthritis, inflammatory bowel disease, Crohn's disease,
 CC acquired immunodeficiency syndrome (AIDS), cancers such as colon cancer
 CC and adenocarcinoma, asthma, hypertension, autoimmune disease, diabetes,
 CC obesity, graft versus host disease, ulcer, bulimia, anorexia and
 CC dementia. Sequences ABG70285-ABG70305 represent human novel polypeptides
 CC of the invention
 XX

SQ Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 5; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.le-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTVIF 60
 Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPLKMHYLPVIYGIIFLVGPGNAVISTVIF 60

Qy 61 KMRPKSSTIIMLNACTDILYLSLPPLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120
 Db 61 KMRPKSSTIIMLNACTDILYLSLPPLIHYYASGENWIFGDFMCKEIRSFHENLYSS 120

Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180
 Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAVIPMTFLTITSTNRNR 180

Qy 181 SACLDTSSDELNTIKWNLLITATTFCPLVIVTVLCVTTIHTLTHGLQDSCILKQKAR 240
 Db 181 SACLDTSSDELNTIKWNLLITATTFCPLVIVTVLCVTTIHTLTHGLQDSCILKQKAR 240

Qy 241 RLTIILLAFVVCFLPFIHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 Db 241 RLTIILLAFVVCFLPFIHILVRIRIESRLLSISCSIEHQIHEAYIVSRPLAALNTFGNLL 300

Qy 301 LYVVSDNFQAVGSTVRCKVSGNLEQAKKISYNNP 337
 Db 301 LYVVSDNFQAVGSTVRCKVSGNLEQAKKISYNNP 337

RESULT 14
 ABP71377
 ID ABP71377 standard; protein; 337 AA.

XX ABP71377;
 AC ABP71377;
 XX

28-APR-2003 (first entry)
Human TGR164 protein.
G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343; TGR358; antisthmatic; neuroprotective; cerebroprotective; nephroretroic; anticonvulsant; hypotensive; hepatotropic; dermatological; human; immunosuppressive; antiinflammatory.
Homo sapiens.
W02003004678-A2.
16-JAN-2003.
01-JUL-2002; 2002WO-US020860.
03-JUL-2001; 2001US-0302800P.
(TULA-) TULARIK INC.
Tian H, Dai K, Chen J, Zhao J, Cutler G;
WPI; 2003-210368/20.
N-PSDB; ABZ59170.
New G-protein coupled receptor polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs for treating or preventing e.g. asthma, multiple sclerosis, stroke or nephrolithiasis.
Claim 17; Page 61; 74pp; English.
The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding polynucleotides. The polypeptides can be expressed by standard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as targets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, asymptomatic urinary abnormalities, hypertension, nephrolithiasis, cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute inflammatory dermatoses. The present sequence represents a human TGR164 protein
Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDVLNADSPDYAAAFNGCTDNIPDKMYLPIVYIGIIFLVGPGNAVVISYIF 60
DB 1 MNEPLDVLNADSPDYAAAFNGCTDNIPDKMYLPIVYIGIIFLVGPGNAVVISYIF 60
QY 61 KMRPWKSTIIMLNACTDILLYLTLPLHYVAGSNGWIFGDFMCKFIKPSHFHLYSS 120
DB 61 KMRPWKSTIIMLNACTDILLYLTLPLHYVAGSNGWIFGDFMCKFIKPSHFHLYSS 120
QY 121 ILFLTCSIFRYCVIHPMCSFISHKTRCAVCAVAVVMIISLNAVIMPTFLTSTNTR 180
DB 121 ILFLTCSIFRYCVIHPMCSFISHKTRCAVCAVAVVMIISLNAVIMPTFLTSTNTR 180
QY 181 SACLDTSSDELNTIKWYNILITATTCPLPIVITLCYITIIHTLHGLQDSCIKQAR 240
DB 181 SACLDTSSDELNTIKWYNILITATTCPLPIVITLCYITIIHTLHGLQDSCIKQAR 240
QY 241 RLTIILLALFVVCPLPHILRVIRIESRLISCSIEHQHEAVIVSRPLAALNTFGNLL 300
DB 241 RLTIILLALFVVCPLPHILRVIRIESRLISCSIEHQHEAVIVSRPLAALNTFGNLL 300

301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337
|||||
301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337
|||||
RESULT 15
ADC26010
ID ADC26010 standard; protein; 337 AA.
XX
AC ADC26010;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human purinergic receptor P2Y-related GPCR10 alternative protein.
XX
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
KW anorectic; cardiant; hypotensive; osteopathic; antianginal;
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW human; GPCR10; purinergic receptor P2Y; chromosome 13.
XX
OS Homo sapiens.
XX
PN US2003088080-A1.
XX
PD 08-MAY-2003.
XX
XX 21-JUN-2001; 2001US-00885453.
XX
PR 20-JUN-2000; 2000US-0212908P.
PR 05-DEC-2000; 2000EP-00870289.
XX
XX (COMM//) COMMUNI D.
XX (LANN//) LANNON V.
XX (GOVA//) GOVAERTS C.
XX (PARM//) PARMENTIER M.
XX (DETH//) DETHOUX M.
XX
XX Communi D, Lannoy V, Govaerts C, Parmentier M, Dethoux M;
WPI; 2003-657983/62.
DR N-PSDB; ADC25997.
XX
XX New human G-protein coupled receptor, useful for treating receptor-mediated disorders, e.g. infections, cancer, pain, diabetes, obesity, acute heart failure, osteoporosis, stroke, ulcer, allergy, or neurological disorders.
XX
XX Claim 6; Page 15; 24pp; English.
XX
XX The invention relates to a novel G-protein coupled receptor (GPCR). The receptor, polynucleotide, agonist, reverse agonist and antagonist of the invention may be useful for treating receptor-mediated disorders including viral, fungal or bacterial infections, immune-related disorders such as cancer, pain, diabetes, obesity, anorexia, acute heart failure, hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke, ulcer and allergy, as well as psychotic and neurological disorders such as schizophrenia and dementia, degenerative diseases such as Parkinson's disease and Alzheimer's disease and dyskinesias such as Huntington's disease. The current sequence is that of the human purinergic receptor P2Y-related GPCR10 alternative protein of the invention which is encoded by DNA located on chromosome 13.
XX
XX Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MNEPLDYLANASDPDYAAAFNGCTDENIPDKHYPVYIYGIIFLVGPGNAVVIITYIF 60
Db 1 MNEPLDYLANASDPDYAAAFNGCTDENIPDKHYPVYIYGIIFLVGPGNAVVIITYIF 60
Qy 61 KMRPWKSTIIIMNLACTDLLYLTSLPFLIHYASGENWIFGDMCKFIRFSHFNYLYSS 120
Db 61 KMRPWKSTIIIMNLACTDLLYLTSLPFLIHYASGENWIFGDMCKFIRFSHFNYLYSS 120
Qy 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAIIPMTFLITSTNRTNR 180
Db 121 ILFLTCSIFRYCVIIHPMSCFSIHKTRCAVAVVWIIISLVAIIPMTFLITSTNRTNR 180
Qy 181 SACLDLTSSDELNTIKWYNLILTATTCLPLVIVTLCYTTIIHTLTHGLOTDSCLKOKAR 240
Db 181 SACLDLTSSDELNTIKWYNLILTATTCLPLVIVTLCYTTIIHTLTHGLOTDSCLKOKAR 240
Qy 241 RLTIILLALLAFVVCPLPFIHLRVIRIESRLISCSISQHEAVIVSRPLAALNTFGNLL 300
Db 241 RLTIILLALLAFVVCPLPFIHLRVIRIESRLISCSISQHEAVIVSRPLAALNTFGNLL 300
Qy 301 LYVVSDNFQOAVCSTVRCKVSGNLEOAKKISYNNP 337
Db 301 LYVVSDNFQOAVCSTVRCKVSGNLEOAKKISYNNP 337

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Search completed: October 29, 2004, 15:01:15

Job time : 163 secs

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